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(54) Title: **DIAGNOSIS OF HYPERINSULINEMIA AND TYPE II DIABETES AND PROTECTION AGAINST SAME**

(57) Abstract: Mouse genes differentially expressed in comparisons of normal vs. hyperinsulinemic, hyperinsulinemic vs. type 2 diabetic, and normal vs. type 2 diabetic liver by gene chip analysis have been identified, as have corresponding human genes and proteins. The human molecules, or antagonists thereof, may be used for protection against hyperinsulinemia or type 2 diabetes, or their sequelae.



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DIAGNOSIS OF HYPERINSULINEMIA AND TYPE II DIABETES AND PROTECTION AGAINST SAME

This application claims the benefit under 35 USC 119(e) of
prior U.S. provisional applications 60/460,415, filed April
7, 2003 (KOPCHICK6-USA), and 60/506,716, filed Sept. 30,
2003 (KOPCHICK6.1-USA), both of which are hereby
incorporated by reference in their entirety.

Cross-Reference to Related Applications

The instant application adds 6 month expression data to
the disclosure of US Prov. Appl. 60/460,415, filed April 7,
2003 (KOPCHICK6-USA).

In U.S. Provisional Appl. Ser. No. 60/458,398 (our
docket Kelder1-USA), filed March 31, 2003, we describe the
identification of genes differentially expressed in normal
vs. hyperinsulinemic, hyperinsulinemic vs. type II diabetic,
or normal vs. type II diabetic mouse liver. Forward- and
reverse-subtracted cDNA libraries were prepared, clones
were isolated, and differentially expressed cDNA inserts
were sequenced and compared with sequences in publicly
available sequence databases. The corresponding mouse and
human genes and proteins were identified. Favorable
genes/proteins so identified included (1) NP_000767: cytochrome
P450, subfamily IIIA (naphthepine oxidase), polypeptide 3; (2) AAG31034:
SYT/SSX4 fusion protein ; and (3) NP_003158: sulfotransferase family,
cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1;
sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring,
member 1. Unfavorable proteins included (4) NP_004884: H2A
histone family, member Y isoform 2; histone macroH2A1.2; histone
macroH2A1.1; (5) AAH37738: Unknown (protein for MGC:33851); (6)
NP_068839: integral membrane protein 2B ; (7) CAA28659: S-protein ;
and (8) AAA51560: alpha-1-antichymotrypsin precursor. Mixed
proteins included (9) NP_000769: cytochrome P450, subfamily IVA,
polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1
monooxygenase; lauric acid omega-hydroxylase; (10) NP_006206: serine (or
cysteine) proteinase inhibitor, clade A ; (11) NP_004489: one cut
domain, family member 1; hepatocyte nuclear factor 6, alpha; and (12)
NP_775491: liver-specific uridine phosphorylase. Gene chip

technology was not used. Two of the genes (NM_007818 and NM_007822) were also identified in the present case.

The use of differential hybridization to identify genes and proteins is also described in our Ser. No. PCT/US00/12145 (Kopchick 3A-PCT), Ser. No. PCT/US00/12366 (Kopchick4A-PCT), and Ser. No. 60/400,052 (Kopchick5). All of the above applications are incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

Field of the Invention

The invention relates to various nucleic acid molecules and proteins, and their use in (1) diagnosing hyperinsulinemia and type II diabetes, or conditions associated with their development, and (2) protecting mammals (including humans) against them.

Description of the Background Art

Diabetes

Diabetes mellitus is a pleiotropic disease of great complexity. The two major types have been termed type I or insulin-dependent diabetes mellitus (IDDM) and type II or non-insulin-dependent diabetes mellitus (NIDDM). Type II diabetes is the predominant form found in the Western world; fewer than 8% of diabetic Americans have the type I disease.

Type I diabetics are often characterized by their low or absent levels of circulating endogenous insulin, i.e., hypoinsulinemia (1). Islet cell antibodies causing damage to the pancreas are frequently present at diagnosis. Injection of exogenous insulin is required to prevent ketosis and sustain life.

Early Type II diabetics are often characterized by hyperinsulinemia and resistance to insulin. Late Type II diabetics may be normoinsulinemic or hypoinsulinemic. Type II diabetics are usually not insulin dependent or prone to ketosis under normal circumstances.

Type II Diabetes

Type II diabetes (formerly known as non-insulin dependent diabetes, NIDDM) is the most common form of

elevated blood glucose (hyperglycemia). Type II diabetes is a metabolic disorder that affects approximately 17 million Americans. It is estimated that another 10 million individuals are "prone" to becoming diabetic. These vulnerable individuals can become resistant to insulin, a pancreatic hormone that signals glucose (blood sugar) uptake by fat and muscle. In order to maintain normal glucose levels, the islet cells of the pancreas produce more insulin, resulting in a condition called hyperinsulinemia. When the pancreas can no longer produce enough insulin to compensate for the insulin resistance, and thereby maintain normal glucose levels, Type II diabetes (hyperglycemia) results.

Complications of diabetes (end organ damage) include retinopathy, neuropathy, and nephropathy (traditionally designated as microvascular complications) as well as atherosclerosis (a macrovascular complication).

Early stages of hyperglycemia can usually be controlled by an alteration in diet and increasing the amount of exercise, but drug treatment, including insulin, may be required. It has been shown that meticulous blood glucose control can often slow down or halt the progression of diabetic complications if caught early enough (1). However, tight metabolic control is extremely difficult to achieve.

Little is known about the disease progression from the normoinsulinemic state to the hyperinsulinemic state, and from the hyperinsulinemic state to the Type II diabetic state.

As stated above, type II diabetes is a metabolic disorder that is characterized by insulin resistance and impaired glucose-stimulated insulin secretion (2,3,4). However, Type II diabetes and atherosclerotic disease are viewed as consequences of having the insulin resistance syndrome (IRS) for many years (5). The current theory of the pathogenesis of Type II diabetes is often referred to as the "insulin resistance/islet cell exhaustion" theory. According to this theory, a condition causing insulin

resistance compels the pancreatic islet cells to hypersecrete insulin in order to maintain glucose homeostasis. However, after many years of hypersecretion, the islet cells eventually fail and the symptoms of clinical diabetes are manifested. Therefore, this theory implies that, at some point, peripheral hyperinsulinemia will be an antecedent of Type II diabetes. Peripheral hyperinsulinemia can be viewed as the difference between what is produced by the β cell minus that which is taken up by the liver. Therefore, peripheral hyperinsulinemia can be caused by increased β cell production, decreased hepatic uptake or some combination of both. It is also important to note that it is not possible to determine the origin of insulin resistance once it is established since the onset of peripheral hyperinsulinemia leads to a condition of global insulin resistance.

Multiple environmental and genetic factors are involved in the development of insulin resistance, hyperinsulinemia and type II diabetes. An important risk factor for the development of insulin resistance, hyperinsulinemia and type II diabetes is obesity, particularly visceral obesity (6,7,8). Type II diabetes exists world-wide, but in developed societies, the prevalence has risen as the average age of the population increases and the average individual becomes more obese.

Obesity is a serious and growing problem in the United States. Obesity-related health risks include high blood pressure, hardening of the arteries, cardiovascular disease, and Type II diabetes (also known as non-insulin-dependent diabetes mellitus, Type II diabetes) (9,10,11). Recent studies show that 85% of the individuals with Type II diabetes are obese (12).

Growth Hormone

Growth hormone has many roles, ranging from regulation of protein, fat and carbohydrate metabolism to growth promotion. GH is produced in the somatotropic cells of the

anterior pituitary and exerts its effects either through the GH-induced action of IGF-I, in the case of growth promotion, or by direct interaction with the GHR on target cells including liver, muscle, adipose, and kidney cells.

5 Hyposecretion of GH during development leads to dwarfism, and hypersecretion before puberty leads to gigantism. In adults, hypersecretion of GH results in acromegaly, a clinical condition characterized by enlarged facial bones, hands, feet, fatigue and an increase in weight. Of those
10 individuals with acromegaly, 25% develop type II diabetes. This may be due to insulin resistance caused by the high circulating levels of GH leading to high circulating levels of insulin (Kopchick et al., Annual Rev. Nutrition 1999. 19:437-61).

15 A further mode of GH action may be through the transcriptional regulation of a number of genes contributing to the physiological effects of GH.

20 *Transgenic Mice*

McGrane, et al., J. Biol. Chem. 263:11443-51 (1988) and Chen, et al., J. Biol. Chem., 269:15892-7 (1994) describe the genetic engineering of mice to express bovine growth hormone (bGH) or human growth hormone (hGH), respectively.

25 These mice exhibited an enhanced growth phenotype. They also developed kidney lesions similar to those seen in diabetic glomerulosclerosis, see Yang, et al., Lab. Invest., 68:62-70 (1993). Ogueta, et al., J. Endocrinol., 165: 321-8 (2000) reported that transgenic mice expressing bovine GH
30 develop arthritic disorder and self-antibodies.

Growth hormone genes and the proteins encoded by them can be converted into growth hormone antagonists by mutation, see Kopchick USP 5,350,836. Transgenic mice have been made that express the GH antagonists bGH-G119R or hGH
35 G120R, and which exhibit a dwarf phenotype. Chen, et al., J. Biol. Chem., 263:15892-7 (1994); Chen, et al., Mol. Endocrinol, 5:1845-52 (1991); Chen, et al., Proc. Nat. Acad. Sci. USA 87:5061-5 (1990). These mice did not develop

kidney lesions. See Yang (1993), supra.

Chen, et al., Endocrinol, 136:660-7 (1995) compared the effect of streptozotocin treatment in normal nontransgenic mice, and in mice transgenic for (1) a GH receptor.

5 antagonist, the G119R mutant of bovine growth hormone or (2) the E117L-mutant of bGH. (According to Chen's ref. 24, these large GH transgenic streptozotocin-treated mice constitute an animal model for diabetes.)

10 Glomerulosclerosis was seen in diabetic (STZ-treated) nontransgenic mice and in diabetic bGH-E117L mice, but not in diabetic bGH-G119R (GH antagonist) mice.

Two of the proteins which mediate growth hormone activity are the growth hormone receptor and the growth hormone binding protein, encoded by the same gene in mice (GHR/BP). It is possible to genetically engineer mice so that the gene encoding these proteins is disrupted ("knocked-out"; inactivated), see Zhou, et al., Proc. Nat. Acad. Sci. (USA), 94:13215-20 (1997). Zhou, et al. inactivated the GHR/BP gene by replacing the 3' portion of exon 4 (which encodes a portion of the GH binding domains) and the 5' region of intron 4 with a neomycin gene cassette. The modified gene was introduced into the target mice by homologous recombination. Like mice expressing a GH antagonist, homozygous GHR/BP-KO mice exhibit a dwarf phenotype. GHR/BP-KO mice, made diabetic by streptozotocin treatment, are protected from the development of diabetes-associated nephropathy. Bellush, et al., Endocrinol., 141:163-8 (2000).

Differential/Subtractive Hybridization

30 Zhang, et al., Kidney International, 56:549-558 (1999) identified genes up-regulated in 5/6 nephrectomized (subtotal renal ablation) mouse kidney by a PCR-based subtraction method. Ten known and nine novel genes were identified. The ultimate goal was to identify genes involved in glomerular hyperfiltration and hypertrophy.

35 Melia, et al., Endocrinol., 139:688-95 (1998) applied

subtractive hybridization methods for the identification of androgen-regulated genes in mouse kidney. The treatment mice were dosed with dihydrotestosterone, an androgen.

Kidney androgen-regulated protein gene was used as a positive control, as it is known to be up-regulated by DHT.

See also Holland, et al., Abstract 607, "Identification of Genes Possibly Involved in Nephropathy of Bovine Growth Hormone Transgenic Mice" (Endocrine Society Meeting, June 22, 2000) and Coschigano, et al., Abstract 333,

"Identification of Genes Potentially Involved in Kidney Protection During Diabetes" (Endocrine Society Meeting, June 22, 2000).

The following differential hybridization articles may also be of interest:

Wada, et al., "Gene expression profile in streptozotocin-induced diabetic mice kidneys undergoing glomerulosclerosis", *Kidney Int.*, 59:1363-73 (2001);

Song, et al., "Cloning of a novel gene in the human kidney homologous to rat munc13S: its potential role in diabetic nephropathy", *Kidney Int.*, 53:1689-95 (1998);

Page, et al., "Isolation of diabetes-associated kidney genes using differential display", *Biochem. Biophys. Res. Comm.*, 232:49-53 (1997).

Peradi, "Subtractive hybridization claims: An efficient technique to detect overexpressed mRNAs in diabetic nephropathy," *Kidney Int.* 53:926-31 (1998).

Condorelli, *EMBO J.*, 17:3858-66 (1998).

See also WO00/66784 (differential hybridization screening for brown adipose tissue); PCT/US00/12366, filed May 5, 2000 (differential hybridization screening for liver).

Identification of genes involved in hyperinsulinemia and type II diabetes

High-fat diets have been shown to induce both obesity and Type II diabetes in laboratory animals (13). Surwit and colleagues demonstrated that male C57BL/6J mice are extremely sensitive to the diabetogenic effects of a high-

fat diet when initiated at weaning. At six months of age, high-fat fed animals had significantly elevated fasting blood-glucose and insulin levels and also demonstrated a decrease in insulin sensitivity (14). Ahren and colleagues
5 (15) reported evidence of insulin resistance as well as diminished glucose-stimulated insulin release, after feeding with a high-fat diet for 12 weeks. These mice also showed elevated levels of total cholesterol, triglycerides, and free fatty acids, another hallmark of Type II diabetes.

10 Our attention recently has focused on the generation of liver mRNA expression profiles and the identification of genes involved in the genesis of the obesity-induced hyperinsulinemia and type-II diabetes. To date, no one has attempted to study the actual progression from the normal
15 condition to that of hyperinsulinemia or from hyperinsulinemia to Type II diabetes in an attempt to identify genes that are up-regulated or down-regulated as the disease progresses.

In previous studies aimed at identifying genes involved
20 in diabetes-induced glomerulosclerosis, differential display and traditional subtractive hybridization techniques were used (16-20). While effective for the identification of a few genes (e.g. hmunc13, PED/PEA-15, lactate dehydrogenase, amiloride sensitive sodium channel, ubiquitin-like protein,
25 mdrl, and α -amyloid protein precursor as well as a few novel genes), these techniques can be quite labor intensive. The PCR-based method of subtractive hybridization requires less starting material, and allows the simultaneous isolation of all differentially expressed cDNAs into two
30 groups (up-regulated and down-regulated).

However, the PCR-based method of subtractive hybridization is also quite labor-intensive, produced large numbers of false positive candidates and ultimately resulted in the identification of a relatively limited number of
35 differentially expressed genes. (see Kelder1-USA application).

In order to expand the number of genes that can be analyzed simultaneously, several groups have begun to

utilize DNA microarray analysis to measure differences in gene expression between normal and diseased states.

However, these experiments have been limited in regards to the number of experimental conditions analyzed. DNA

5 microarray analysis has been performed on normal, obese and diabetic mice (21). Also, the obesity and diabetes in the mouse models examined were caused by a specific endogenous genetic mutation (22). The differentially expressed genes in the above models may be very different from genes
10 differentially expressed due to diet-induced obesity and Type-II diabetes.

SUMMARY OF THE INVENTION

Differential hybridization techniques have been used to identify mouse genes that are differentially expressed in mice, depending upon their development of hyperinsulinemia or type II diabetes.

In essence, complementary RNA derived from normal mice, or mouse models of hyperinsulinemia or type II diabetes, was screened for hybridization with oligonucleotide probes each specific to a particular mouse gene, each gene in turn representative of a particular mouse gene cluster (Unigene). Mouse genes which were differentially expressed (normal vs. hyperinsulinemic, hyperinsulinemic vs. diabetic, or normal vs. diabetic), as measured by different levels of hybridization of the respective cRNA samples with the particular probe corresponding to that mouse gene) were identified. Related human genes and proteins were identified by sequence comparisons to the mouse gene or protein.

After identifying related human genes and proteins, one may formulate agents useful in screening humans at risk for progression toward hyperinsulinemia or toward type II diabetes.

Since the progression is from normal to hyperinsulinemic, and thence from hyperinsulinemic to type II diabetic, one may define mammalian subjects as being more favored or less favored, with normal subjects being more favored than hyperinsulinemic subjects, and hyperinsulinemic subjects being more favored than type II diabetic subjects. The subjects' state may then be correlated with their gene expression activity.

Thus, "favorable" human genes/proteins are defined as those corresponding to mouse genes which were less strongly expressed in mouse hyperinsulinemic liver than in control liver, or less strongly expressed in mouse type II diabetic liver than in hyperinsulinemic liver. (The control liver is the liver of a mouse which is normal vis-a-vis fasting insulin and fasting glucose levels. The term "normal", as

used herein, means normal relative to those parameters, and does not necessitate that the mouse be normal in every respect.) Likewise, one may define "unfavorable" human genes/proteins as those corresponding to mouse genes which were more strongly expressed in mouse hyperinsulinemic liver than in control liver, or more strongly expressed in mouse type II diabetic liver than in hyperinsulinemic liver.

As used herein, the term "corresponding" does not mean identical, but rather implies the existence of a statistically significant sequence similarity, such as one sufficient to qualify the human protein or gene as a homologous protein or DNA as defined below. The greater the degree of relationship as thus defined (i.e., by the statistical significance of each alignment used to connect the mouse cDNA to the human protein or gene, measured by an E value), the more close the correspondence. The connection may be direct (mouse gene to human protein) or indirect (e.g., mouse gene to human gene, human gene to human protein). By "mouse gene", we mean the mouse gene from which the gene chip DNA in question was derived.

In general, the human genes/proteins which most closely correspond, directly or indirectly, to the mouse genes are preferred, such as the one(s) with the highest, top two highest, top three highest, top four highest, top five highest, and top ten highest E values for the final alignment in the connection process. The human genes/proteins deemed to correspond to our mouse cDNA clones are identified in the Master Tables.

A human gene/protein corresponding to a mouse cDNA which was more strongly expressed in hyperinsulinemic liver than in either normal or type II diabetic liver (i.e., $C < HI$, $HI > D$) will be deemed both "unfavorable", by virtue of the control:hyperinsulinemic comparison, and "favorable", by virtue of the hyperinsulinemic:diabetic comparison. This is one of several possible "mixed" expression patterns.

Thus, we can subdivide the "favorables" into wholly and partially favorables. Likewise, we can subdivide the unfavorables into wholly and partially unfavorables. The

genes/proteins with "mixed" expression patterns are, by definition, both partially favorable and partially unfavorable. In general, use of the wholly favorable or wholly unfavorable genes/proteins is preferred to use of the partially favorable or partially unfavorable ones.

Agents which bind the "favorable" and "unfavorable" nucleic acids (e.g., the agent is a substantially complementary nucleic acid hybridization probe), or the corresponding proteins (e.g., an antibody vs. the protein) may be used to evaluate whether a human subject is at increased or decreased risk for progression toward type II diabetes. A subject with one or more elevated "unfavorable" and/or one or more depressed "favorable" genes/proteins is at increased risk, and one with one or more elevated "favorable" and/or one or more depressed "unfavorable" genes/proteins is at decreased risk. One may further take into account whether the subject is normoinsulinemic or hyperinsulinemic at the time of the assay. If the subject is non-diabetic and normoinsulinemic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in hyperinsulinemic vs. normal livers. If the subject is already hyperinsulinemic, yet non-diabetic, we are especially interested in the "favorable" and "unfavorable" genes/proteins corresponding to mouse genes differentially expressed in type II diabetic vs. hyperinsulinemic livers.

The assay may be used as a preliminary screening assay to select subjects for further analysis, or as a formal diagnostic assay.

The identification of the related genes and proteins may also be useful in protecting humans against these disorders.

Thus, Applicants contemplate:

(1) use of the "favorable" mouse DNAs of the Master Tables (below) to isolate or identify related human DNAs;

(2) use of human DNAs, related to favorable mouse DNAs, to express the corresponding human proteins;

5 (3) use of the corresponding human proteins (and mouse proteins, if biologically active in humans), to protect against the disorder(s);

(4) use of the corresponding mouse or human proteins, or nucleic acid probes derived from the mouse or human
10 genes, in diagnostic agents, in assays to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage; and

(5) use of the corresponding human or mouse genes
15 therapeutically in gene therapy, to protect against the disorder(s).

Moreover Applicants contemplate:

(1) use of the "unfavorable" mouse DNAs of the Master Tables to isolate or identify related human DNAs;

20 (2) use of the complement to the "unfavorable" mouse DNAs or related human DNAs, as antisense molecules to inhibit expression of the related human DNAs;

(3) use of the mouse or human DNAs to express the corresponding mouse or human proteins;

25 (4) use of the corresponding mouse or human proteins, in diagnostic agents, to measure progression toward hyperinsulinemia or type II diabetes, or protection against the disorder(s), or to estimate related end organ damage such as kidney damage;

30 (5) use of the corresponding mouse or human proteins in assays to determine whether a substance binds to (and hence may neutralize) the protein; and

(6) use of the neutralizing substance to protect against the disorder(s).

35 The related human DNAs may be identified by comparing the mouse sequence (or its AA translation product) to known human DNAs (and their AA translation products). If this is unsuccessful, human cDNA or genomic DNA libraries may be

screened using the mouse DNA as a probe.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS OF THE INVENTION

Subjects

5 A mouse is considered to be a diabetic subject if, regardless of its fasting plasma insulin level, it has a fasting plasma glucose level of at least 190 mg/dL. A mouse is considered to be a hyperinsulinemic subject if its
10 fasting plasma insulin level is at least 0.67 ng/mL and it does not qualify as a diabetic subject. A mouse is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very limited manner.

15 A mouse is considered "obese" if its weight is at least 15% in excess of the mean weight for mice of its age and sex. A mouse which does not satisfy this standard may be characterized as "non-obese", the term "normal" being reserved for use in reference to glucose and insulin levels as previously described.

20 A human is considered a diabetic subject if, regardless of his or her fasting plasma insulin level, the fasting plasma glucose level is at least 126 mg/dL. A human is considered a hyperinsulinemic subject if the fasting plasma
25 insulin level is more than 26 micro International Units/mL (it is believed that this is equivalent to 1.08 ng/mL), and does not qualify as a diabetic subject. A human is considered to be "normal" if it is neither diabetic nor hyperinsulinemic. Thus, normality is defined in a very
30 limited manner.

A human is considered "obese" if the body mass index (BMI) (weight divided by height squared) is at least 30 kg/m². A human who does not satisfy this standard may be characterized as "non-obese", the term "normal" being
35 reserved for use in reference to glucose and insulin levels as previously described.

A human is considered overweight if the BMI is at least 25 kg/m². Thus, we define overweight to include obese

individuals, consistent with the recommendations of the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK). A human who does not satisfy this standard may be characterized as "non-overweight."

5

According to the Report of the Expert Committee on the Diagnosis and Classification of Diabetes Mellitus, Diabetes Care 20: 1183-97 (1997), the following are risk factors for diabetes type II:

10

older (e.g., at least 45; see below)

excessive weight (see below)

15

first-degree relative with diabetes mellitus

member of high risk ethnic group (black, Hispanic, Native American, Asian)

20

history of gestational diabetes mellitus or delivering a baby weighing more than 9 pounds (4.032 kg)

hypertensive (>140/90 mm Hg)

25

HDL cholesterol level >35 mg/dL (0.90 mmol/L)

triglyceride level \geq 250 mg/dL (2.83 mmol/L)

30

Hence, in a preferred embodiment, the diagnostic and protective methods of the present invention are applied to human subjects exhibiting one or more of the aforementioned risk factors. Likewise, in a preferred embodiment, they are applied to human subjects who, while not diabetic, exhibit impaired glucose homeostasis (110 to <126 mg/dL).

35

The risk of diabetes increases with age. Hence, in successive preferred embodiments, the age of the subjects is at least 45, at least 50, at least 55, at least 60, at least

65, at least 70, and at least 75.

With regard to excessive weight, NIDDK says that "The relative risk of diabetes increases by approximately 25 percent for each additional unit of BMI over 22." Hence, in successive preferred embodiments, the BMIs of the human subjects is at least 23, at least 24, at least 25 (i.e., overweight by our criterion), at least 26, at least 27, at least 28, at least 29, at least 30 (i.e., obese), at least 31, at least 32, at least 33, at least 34, at least 35, at least 36, at least 37, at least 38, at least 39, at least 40, or over 40.

Genes/Proteins of Interest

Favorable genes/proteins are those corresponding to genes less strongly expressed in hyperinsulinemic liver than in normal liver, or in type II diabetic liver as compared to hyperinsulinemic liver. Unfavorable genes/proteins are those corresponding to genes more strongly expressed in hyperinsulinemic liver than in normal liver, or in type II diabetic liver as compared to hyperinsulinemic liver.

Mixed genes/proteins are those exhibiting a combination of favorable and unfavorable behavior. A mixed gene/protein can be used as would a favorable gene/protein if its favorable behavior outweighs the unfavorable. It can be used as would an unfavorable gene/protein if its unfavorable behavior outweighs the favorable. Preferably, they are used in conjunction with other agents that affect their balance of favorable and unfavorable behavior. Use of mixed genes/proteins is, in general, less desirable than use of purely favorable or purely unfavorable genes/proteins.

For each of the differentially expressed genes, corresponding mouse and human proteins have been identified, as set forth in the Master Tables.

Direct and Indirect Utility of Identified Nucleic Acid

Sequences and Related Molecules

The mouse or human genes (or fragments thereof) may be used directly. For diagnostic or screening purposes, they (or specific binding fragments thereof) may be labeled and
5 used as hybridization probes. For therapeutic purposes, they (or specific binding fragments thereof) may be used as antisense reagents to inhibit the expression of the corresponding gene, or of a sufficiently homologous gene of another species.

10 Since each of the probes is representative of a full-length mouse gene, that is, it encodes an entire, functional protein, then it may be used in the expression of that protein. Likewise, if the corresponding human gene is known in full-length, it may be used to express the human protein.
15 Such expression may be in cell culture, with the protein subsequently isolated and administered exogenously to subjects who would benefit therefrom, or in vivo, i.e., administration by gene therapy. Naturally, any DNA encoding the same protein, or a fragment or a mutant protein which
20 retains the desired activity, may be used for the same purpose. The encoded protein of course has utility therapeutically and, in labeled or immobilized form, diagnostically.

The genes may also be used indirectly, that is, to
25 identify other useful DNAs, proteins, or other molecules.

There thus are several ways that a human protein homologue of interest can be identified by database searching, including:

30 1) a DNA->DNA (BlastN) search for database DNAs closely related to the mouse gene identifies a known human gene, and the sequence of the human protein is deduced by the Genetic Code;

35 2) a DNA->Protein (BlastX) search for database proteins closely related to the translated DNA of the mouse gene identifies a known human protein; and

3) the sequence of the mouse protein is known or is deduced by the Genetic Code, and a Protein->Protein (BlastP) search for closely related database proteins identifies a known human protein.

5 Once a known human gene is identified, it may be used in further BlastN or BlastX searches to identify other human genes or proteins. Once a known human protein is identified, it may be used in further BlastP searches to
10 identify other human proteins.

Searches may also take cognizance, intermediately, of known genes and proteins other than mouse or human ones, e.g., use the mouse sequence to identify a known rat sequence and then
15 the rat sequence to identify a human one.

Thus, if we have identified a mouse gene, and it encodes a mouse protein which appears similar to a human protein, then that human protein may be used (especially in
20 humans) for purposes analogous to the proposed use of the mouse protein in mice. Moreover, a specific binding fragment of an appropriate strand of the corresponding human gene or cDNA could be labeled and used as a hybridization probe (especially against samples of human mRNA or cDNA).

25 In determining whether the disclosed genes have significant similarities to known DNAs (and their translated AA sequences to known proteins), one would generally use the disclosed gene as a query sequence in a search of a sequence database. The results of several such searches are set
30 forth in the Examples. Such results are dependent, to some degree, on the search parameters. Preferred parameters are set forth in Example 1. The results are also dependent on the content of the database. While the raw similarity score of a particular target (database) sequence will not vary
35 with content (as long as it remains in the database), its informational value (in bits), expected value, and relative ranking can change. Generally speaking, the changes are small.

It will be appreciated that the nucleic acid and protein databases keep growing. Hence a later search may identify high scoring target sequences which were not uncovered by an earlier search because the target sequences were not previously part of a database.

Hence, in a preferred embodiment, the cognate DNAs and proteins include not only those set forth in the examples, but those which would have been highly ranked (top ten, more preferably top three, even more preferably top two, most preferably the top one) in a search run with the same parameters on the date of filing of this application.

If the known human DNA is appears to be a partial DNA, it may be used as a hybridization probe to isolate the full-length DNA. If the partial DNA encodes a biologically functional fragment of the cognate protein, it may be used in a manner similar to the full length DNA, i.e., to produce the functional fragment.

If we have indicated that an antagonist of a protein or other molecule is useful, then such an antagonist may be obtained by preparing a combinatorial library, as described below, of potential antagonists, and screening the library members for binding to the protein or other molecule in question. The binding members may then be further screened for the ability to antagonize the biological activity of the target. The antagonists may be used therapeutically, or, in suitably labeled or immobilized form, diagnostically.

If the identified DNA is related to a known protein, then substances known to interact with that protein (e.g., agonists, antagonists, substrates, receptors, second messengers, regulators, and so forth), and binding molecules which bind them, are also of utility. Such binding molecules can likewise be identified by screening a combinatorial library.

Isolation of Full Length cDNAs Using Partial cDNAs as probes

If it is determined that a DNA of the present invention is a partial DNA, and the cognate full length DNA is not listed in a sequence database, the available DNA may be used as a hybridization probe to isolate the full-length cDNA from a suitable cDNA library.

Stringent hybridization conditions are appropriate, that is, conditions in which the hybridization temperature is 5-10 deg. C. below the T_m of the cDNA as a perfect duplex.

Identification and Isolation of Homologous Genes/cDNAs Using a cDNA Probe

It may be that the sequence databases available do not include the sequence of any homologous gene, or at least of the homologous gene for a species of interest. However, given the cDNAs set forth above, one may readily obtain the homologous gene.

The possession of one DNA (the "starting DNA") greatly facilitates the isolation of homologous genes/cDNAs. If only a partial DNA is known, this partial DNA may first be used as a probe to isolate the corresponding full length DNA for the same species, and that the latter may be used as the starting DNA in the search for homologous genes.

The starting DNA, or a fragment thereof, is used as a hybridization probe to screen a cDNA or genomic DNA library for clones containing inserts which encode either the entire homologous protein, or a recognizable fragment thereof. The minimum length of the hybridization probe is dictated by the need for specificity. If the size of the library in bases is L , and the GC content is 50%, then the probe should have a length of at least l , where $L = 4^l$. This will yield, on average, a single perfect match in random DNA of L bases. The human cDNA library is about 10^8 bases and the human genomic DNA library is about 10^{10} bases.

The library is preferably derived from an organism which is known, on biochemical evidence, to produce a homologous protein, and more preferably from the genomic DNA or mRNA of cells of that organism which are likely to be

relatively high producers of that protein. A cDNA library (which is derived from an mRNA library) is especially preferred.

If the organism in question is known to have substantially different codon preferences from that of the organism whose relevant cDNA or genomic DNA is known, a synthetic hybridization probe may be used which encodes the same amino acid sequence but whose codon utilization is more similar to that of the DNA of the target organism.

Alternatively, the synthetic probe may employ inosine as a substitute for those bases which are most likely to be divergent, or the probe may be a mixed probe which mixes the codons for the source DNA with the preferred codons (encoding the same amino acid) for the target organism.

By routine methods, the T_m of a perfect duplex of starting DNA is determined. One may then select a hybridization temperature which is sufficiently lower than the perfect duplex T_m to allow hybridization of the starting DNA (or other probe) to a target DNA which is divergent from the starting DNA. A 1% sequence divergence typically lowers the T_m of a duplex by 1-2°C, and the DNAs encoding homologous proteins of different species typically have sequence identities of around 50-80%. Preferably, the library is screened under conditions where the temperature is at least 20°C., more preferably at least 50°C., below the perfect duplex T_m . Since salt reduces the T_m , one ordinarily would carry out the search for DNAs encoding highly homologous proteins under relatively low salt hybridization conditions, e.g., <1M NaCl. The higher the salt concentration, and/or the lower the temperature, the greater the sequence divergence which is tolerated.

For the use of probes to identify homologous genes in other species, see, e.g., Schwinn, et al., J. Biol. Chem., 265:8183-89 (1990) (hamster 67-bp cDNA probe vs. human leukocyte genomic library; human 0.32kb DNA probe vs. bovine brain cDNA library, both with hybridization at 42°C in 6xSSC); Jenkins et al., J. Biol. Chem., 265:19624-31 (1990) (Chicken 770-bp cDNA probe vs. human genomic libraries;

hybridization at 40°C in 50% formamide and 5xSSC); Murata et al., J. Exp. Med., 175:341-51 (1992) (1.2-kb mouse cDNA probe v. human eosinophil cDNA library; hybridization at 65°C in 6xSSC); Guyer et al., J. Biol. Chem., 265:17307-17 (1990) (2.95-kb human genomic DNA probe vs. porcine genomic DNA library; hybridization at 42°C in 5xSSC). The conditions set forth in these articles may each be considered suitable for the purpose of isolating homologous genes.

10 Homologous Proteins and DNAs

A human protein can be said to be identifiable as homologous to a mouse gene (and hence to "correspond" to such gene) if

15

(1) its sequence can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and the expected value (E) of the alignment (the probability that such an alignment would have occurred by chance alone) is less than e^{-10} ,

20

(2) its sequence can be aligned to a human gene, using BlastX with the default parameters set forth below, and the cDNA of said human gene can be aligned to the mouse gene, using BlastN with the default parameters set forth below, and the E value for both alignments is less than e^{-10} ,

25

(3) its sequence can be aligned to a mouse protein, using BlastP with the default parameters set forth below, and that mouse protein can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and in both alignments the E value of the alignment is less than e^{-10} .

30

Naturally, if the human protein is encoded by the human gene of (2), or the mouse protein is encoded by the mouse gene of (3), the BlastX alignment will be satisfied.

35

Desirably, two or all three of these conditions (1)-(3) are

satisfied.

Preferably, for any of the alignments noted above, and more preferably for all of them, the E value is less than e-15, more preferably less than e-20, still more preferably less than e-40, even more preferably less than e-60, considerably more preferably less than e-80, and most preferably less than e-100. More preferably, for those conditions in which the mouse cDNA clone is indirectly connected to the human protein by virtue of two or more successive alignments, the E value is so limited for all of said alignments in the connecting chain.

BlastN and BlastX report very low expected values as "0.0". This does not truly mean that the expected value is exactly zero (since any alignment could occur by chance), but merely that it is so infinitesimal that it is not reported. The documentation does not state the cutoff value, alignments with explicit E values as low as e-178 (624 bits) have been reported as such, while a score of 636 bits was reported as "0.0".

Functionally homologous human proteins are also of interest. A human protein may be said to be functionally homologous to the mouse gene if (1) it can be aligned to the mouse gene, using BlastX with the default parameters set forth below, and the E value of the alignment is less than e-50, and (2) the human protein has at least one biological activity in common with the mouse protein.

The human proteins of interest also include those that are substantially and/or conservatively identical (as defined below) to the homologous and/or functionally homologous human proteins defined above.

Relevance of Favorable and Unfavorable Genes

If a gene is down-regulated in more favored mammals, or up-regulated in less favored mammals, (i.e., an "unfavorable gene") then several utilities are apparent.

First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject. Elevated levels are indicative of progression, or propensity to progression, to a less favored state, and clinicians may take appropriate preventative, curative or ameliorative action.

Secondly, the messenger RNA product (or equivalent cDNA), the protein product, or a binding molecule specific for that product (e.g., an antibody which binds the product), or a downstream product which mediates the activity (e.g., a signaling intermediate) or a binding molecule (e.g., an antibody) therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said nucleic acid product, protein product, or downstream product (e.g., a signaling intermediate). Again, elevated levels are indicative of a present or future problem.

Thirdly, an agent which down-regulates expression of the gene may be used to reduce levels of the corresponding protein and thereby inhibit further damage. This agent could inhibit transcription of the gene in the subject, or translation of the corresponding messenger RNA. Possible inhibitors of transcription and translation include antisense molecules and repressor molecules. The agent could also inhibit a post-translational modification (e.g., glycosylation, phosphorylation, cleavage, GPI attachment) required for activity, or post-translationally modify the protein so as to inactivate it. Or it could be an agent which down- or up-regulated a positive or negative regulatory gene, respectively.

Fourthly, an agent which is an antagonist of the

messenger RNA product or protein product of the gene, or of a downstream product through which its activity is manifested (e.g., a signaling intermediate), may be used to inhibit its activity.

5 This antagonist could be an antibody, a peptide, a peptoid, a nucleic acid, a peptide nucleic acid (PNA) oligomer, a small organic molecule of a kind for which a combinatorial library exists (e.g., a benzodiazepine), etc. An antagonist is simply a binding molecule which, by
10 binding, reduces or abolishes the undesired activity of its target. The antagonist, if not an oligomeric molecule, is preferably less than 500 daltons.

 Fifthly, an agent which degrades, or abets the degradation of, that messenger RNA, its protein product or a
15 downstream product which mediates its activity (e.g., a signaling intermediate), may be used to curb the effective period of activity of the protein.

 If a gene is up-regulated in more favored mammals, or down-regulated in less favored animals then the utilities
20 are converse to those stated above.

 First, the complementary strand of the gene, or a portion thereof, may be used in labeled form as a hybridization probe to detect messenger RNA and thereby monitor the level of expression of the gene in a subject.
25 Depressed levels are indicative of damage, or possibly of a propensity to damage, and clinicians may take appropriate preventative, curative or ameliorative action.

 Secondly, the messenger RNA product, the equivalent cDNA, protein product, or a binding molecule specific for
30 those products, or a downstream product, or a signaling intermediate, or a binding molecule therefor, may be used, preferably in labeled or immobilized form, as an assay reagent in an assay for said protein product or downstream product. Again, depressed levels are indicative of a
35 present or future problem.

 Thirdly, an agent which up-regulates expression of the gene may be used to increase levels of the corresponding protein and thereby inhibit further progression to a less

5 favored state. By way of example, it could be a vector which carries a copy of the gene, but which expresses the gene at higher levels than does the endogenous expression system. Or it could be an agent which up- or down-regulates a positive or negative regulatory gene.

10 Fourthly, an agent which is an agonist of the protein product of the gene, or of a downstream product through which its activity (of inhibition of progression to a less favored state) is manifested, or of a signaling intermediate may be used to foster its activity.

15 Fifthly, an agent which inhibits the degradation of that protein product or of a downstream product or of a signaling intermediate may be used to increase the effective period of activity of the protein.

Mutant Proteins

20 The present invention also contemplates mutant proteins (peptides) which are substantially identical (as defined below) to the parental protein (peptide). In general, the fewer the mutations, the more likely the mutant protein is to retain the activity of the parental protein. The effect of mutations is usually (but not always) additive. Certain individual mutations are more likely to be tolerated than
25 others.

A protein is more likely to tolerate a mutation which

(a) is a substitution rather than an insertion or deletion;

30 (b) is an insertion or deletion at the terminus, rather than internally, or, if internal, is at a domain boundary, or a loop or turn, rather than in an alpha helix or beta strand;

(c) affects a surface residue rather than an interior residue;

35 (d) affects a part of the molecule distal to the binding site;

(e) is a substitution of one amino acid for another of similar size, charge, and/or

hydrophobicity, and does not destroy a disulfide bond or other crosslink; and

(f) is at a site which is subject to substantial variation among a family of homologous proteins to which the protein of interest belongs.

These considerations can be used to design functional mutants.

Surface vs. Interior Residues

Charged residues almost always lie on the surface of the protein. For uncharged residues, there is less certainty, but in general, hydrophilic residues are partitioned to the surface and hydrophobic residues to the interior. Of course, for a membrane protein, the membrane-spanning segments are likely to be rich in hydrophobic residues.

Surface residues may be identified experimentally by various labeling techniques, or by 3-D structure mapping techniques like X-ray diffraction and NMR. A 3-D model of a homologous protein can be helpful.

Binding Site Residues

Residues forming the binding site may be identified by (1) comparing the effects of labeling the surface residues before and after complexing the protein to its target, (2) labeling the binding site directly with affinity ligands, (3) fragmenting the protein and testing the fragments for binding activity, and (4) systematic mutagenesis (e.g., alanine-scanning mutagenesis) to determine which mutants destroy binding. If the binding site of a homologous protein is known, the binding site may be postulated by analogy.

Protein libraries may be constructed and screened that a large family (e.g., 10^8) of related mutants may be evaluated simultaneously.

Hence, the mutations are preferably conservative modifications as defined below.

"Substantially Identical"

A mutant protein (peptide) is substantially identical to a reference protein (peptide) if (a) it has at least 10% of a specific binding activity or a non-nutritional
5 biological activity of the reference protein, and (b) is at least 50% identical in amino acid sequence to the reference protein (peptide). It is "substantially structurally identical" if condition (b) applies, regardless of (a).

Percentage amino acid identity is determined by
10 aligning the mutant and reference sequences according to a rigorous dynamic programming algorithm which globally aligns their sequences to maximize their similarity, the similarity being scored as the sum of scores for each aligned pair according to an unbiased PAM250 matrix, and a penalty for
15 each internal gap of -12 for the first null of the gap and -4 for each additional null of the same gap. The percentage identity is the number of matches expressed as a percentage of the adjusted (i.e., counting inserted nulls) length of the reference sequence.

20 A mutant DNA sequence is substantially identical to a reference DNA sequence if they are structural sequences, and encoding mutant and reference proteins which are substantially identical as described above.

If instead they are regulatory sequences, they are
25 substantially identical if the mutant sequence has at least 10% of the regulatory activity of the reference sequence, and is at least 50% identical in nucleotide sequence to the reference sequence. Percentage identity is determined as for proteins except that matches are scored +5, mismatches -
30 4, the gap open penalty is -12, and the gap extension penalty (per additional null) is -4.

Preferably, sequence which are substantially identical exceed the minimum identity of 50% e.g., are 51%, 66%, 75%, 80%, 85%, 90%, 95% or 99% identical in sequence.

35 DNA sequences may also be considered "substantially identical" if they hybridize to each other under stringent conditions, i.e., conditions at which the T_m of the heteroduplex of the one strand of the mutant DNA and the

more complementary strand of the reference DNA is not in excess of 10°C. less than the T_m of the reference DNA homoduplex. Typically this will correspond to a percentage identity of 85-90%.

5 "Conservative Modifications"

"Conservative modifications" are defined as

(a) conservative substitutions of amino acids as hereafter defined; or

10 (b) single or multiple insertions (extension) or deletions (truncation) of amino acids at the termini.

Conservative modifications are preferred to other modifications. Conservative substitutions are preferred to
15 other conservative modifications.

"Semi-Conservative Modifications" are modifications which are not conservative, but which are (a) semi-conservative substitutions as hereafter defined; or (b)
20 single or multiple insertions or deletions internally, but at interdomain boundaries, in loops or in other segments of relatively high mobility. Semi-conservative modifications are preferred to nonconservative modifications. Semi-conservative substitutions are preferred to other semi-conservative modifications.

25 Non-conservative substitutions are preferred to other non-conservative modifications.

The term "conservative" is used here in an a priori sense, i.e., modifications which would be expected to preserve 3D structure and activity, based on analysis of the
30 naturally occurring families of homologous proteins and of past experience with the effects of deliberate mutagenesis, rather than post facto, a modification already known to conserve activity. Of course, a modification which is conservative a priori may, and usually is, also conservative
35 post facto.

Preferably, except at the termini, no more than about five amino acids are inserted or deleted at a particular locus, and the modifications are outside regions known to

contain binding sites important to activity.

Preferably, insertions or deletions are limited to the termini.

A conservative substitution is a substitution of one amino acid for another of the same exchange group, the exchange groups being defined as follows

- I Gly, Pro, Ser, Ala (Cys) (and any nonbiogenic, neutral amino acid with a hydrophobicity not exceeding that of the aforementioned a.a.'s)
- II Arg, Lys, His (and any nonbiogenic, positively-charged amino acids)
- III Asp, Glu, Asn, Gln (and any nonbiogenic negatively-charged amino acids)
- IV Leu, Ile, Met, Val (Cys) (and any nonbiogenic, aliphatic, neutral amino acid with a hydrophobicity too high for I above)
- V Phe, Trp, Tyr (and any nonbiogenic, aromatic neutral amino acid with a hydrophobicity too high for I above).

Note that Cys belongs to both I and IV.

Residues Pro, Gly and Cys have special conformational roles. Cys participates in formation of disulfide bonds. Gly imparts flexibility to the chain. Pro imparts rigidity to the chain and disrupts α helices. These residues may be essential in certain regions of the polypeptide, but substitutable elsewhere.

One, two or three conservative substitutions are more likely to be tolerated than a larger number.

"Semi-conservative substitutions" are defined herein as being substitutions within supergroup I/II/III or within supergroup IV/V, but not within a single one of groups I-V. They also include replacement of any other amino acid with alanine. If a substitution is not conservative, it preferably is semi-conservative.

"Non-conservative substitutions" are substitutions which are not "conservative" or "semi-conservative".

"Highly conservative substitutions" are a subset of conservative substitutions, and are exchanges of amino acids

within the groups Phe/Tyr/Trp, Met/Leu/Ile/Val, His/Arg/Lys, Asp/Glu and Ser/Thr/Ala. They are more likely to be tolerated than other conservative substitutions. Again, the smaller the number of substitutions, the more likely they are to be tolerated.

"Conservatively Identical"

A protein (peptide) is conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by conservative modifications, the protein (peptide) remaining at least seven amino acids long if the reference protein (peptide) was at least seven amino acids long.

A protein is at least semi-conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by semi-conservative or conservative modifications.

A protein (peptide) is nearly conservatively identical to a reference protein (peptide) if it differs from the latter, if at all, solely by one or more conservative modifications and/or a single nonconservative substitution.

It is highly conservatively identical if it differs, if at all, solely by highly conservative substitutions. Highly conservatively identical proteins are preferred to those merely conservatively identical. An absolutely identical protein is even more preferred.

The core sequence of a reference protein (peptide) is the largest single fragment which retains at least 10% of a particular specific binding activity, if one is specified, or otherwise of at least one specific binding activity of the referent. If the referent has more than one specific binding activity, it may have more than one core sequence, and these may overlap or not.

If it is taught that a peptide of the present invention may have a particular similarity relationship (e.g., markedly identical) to a reference protein (peptide),

preferred peptides are those which comprise a sequence having that relationship to a core sequence of the reference protein (peptide), but with internal insertions or deletions in either sequence excluded. Even more preferred peptides are those whose entire sequence has that relationship, with the same exclusion, to a core sequence of that reference protein (peptide).

10 Library

The term "library" generally refers to a collection of chemical or biological entities which are related in origin, structure, and/or function, and which can be screened simultaneously for a property of interest.

15 Libraries may be classified by how they are constructed (natural vs. artificial diversity; combinatorial vs. noncombinatorial), how they are screened (hybridization, expression, display), or by the nature of the screened library members (peptides, nucleic acids, etc.).

20 In a "natural diversity" library, essentially all of the diversity arose without human intervention. This would be true, for example, of messenger RNA extracted from a non-engineered cell.

In a "synthetic diversity" library, essentially all of the diversity arose deliberately as a result of human intervention. This would be true for example of a combinatorial library; note that a small level of natural diversity could still arise as a result of spontaneous mutation. It would also be true of a noncombinatorial library of compounds collected from diverse sources, even if they were all natural products.

In a "non-natural diversity" library, at least some of the diversity arose deliberately through human intervention.

35 In a "controlled origin" library, the source of the diversity is limited in some way. A limitation might be to cells of a particular individual, to a particular species, or to a particular genus, or, more complexly, to individuals of a particular species who are of a particular age, sex,

physical condition, geographical location, occupation and/or familial relationship. Alternatively or additionally, it might be to cells of a particular tissue or organ. Or it could be cells exposed to particular pharmacological, environmental, or pathogenic conditions. Or the library could be of chemicals, or a particular class of chemicals, produced by such cells.

In a "controlled structure" library, the library members are deliberately limited by the production conditions to particular chemical structures. For example, if they are oligomers, they may be limited in length and monomer composition, e.g. hexapeptides composed of the twenty genetically encoded amino acids.

Hybridization Library

In a hybridization library, the library members are nucleic acids, and are screened using a nucleic acid hybridization probe. Bound nucleic acids may then be amplified, cloned, and/or sequenced.

Expression Library

In an expression library, the screened library members are gene expression products, but one may also speak of an underlying library of genes encoding those products. The library is made by subcloning DNA encoding the library members (or portions thereof) into expression vectors (or into cloning vectors which subsequently are used to construct expression vectors), each vector comprising an expressible gene encoding a particular library member, introducing the expression vectors into suitable cells, and expressing the genes so the expression products are produced.

In one embodiment, the expression products are secreted, so the library can be screened using an affinity reagent, such as an antibody or receptor. The bound expression products may be sequenced directly, or their sequences inferred by, e.g., sequencing at least the variable portion of the encoding DNA.

In a second embodiment, the cells are lysed, thereby exposing the expression products, and the latter are screened with the affinity reagent.

5 In a third embodiment, the cells express the library members in such a manner that they are displayed on the surface of the cells, or on the surface of viral particles produced by the cells. (See display libraries, below).

10 In a fourth embodiment, the screening is not for the ability of the expression product to bind to an affinity reagent, but rather for its ability to alter the phenotype of the host cell in a particular detectable manner. Here, the screened library members are transformed cells, but there is a first underlying library of expression products which mediate the behavior of the cells, and a second
15 underlying library of genes which encode those products.

Display Library

In a display library, the library members are each conjugated to, and displayed upon, a support of some kind.
20 The support may be living (a cell or virus), or nonliving (e.g., a bead or plate).

If the support is a cell or virus, display will normally be effectuated by expressing a fusion protein which comprises the library member, a carrier moiety allowing
25 integration of the fusion protein into the surface of the cell or virus, and optionally a lining moiety. In a variation on this theme, the cell coexpresses a first fusion comprising the library member and a linking moiety L1, and a second fusion comprising a linking moiety L2 and the carrier
30 moiety. L1 and L2 interact to associate the first fusion with the second fusion and hence, indirectly, the library member with the surface of the cell or virus.

Soluble Library

35 In a soluble library, the library members are free in solution. A soluble library may be produced directly, or one may first make a display library and then release the library members from their supports.

Encapsulated Library

In an encapsulated library, the library members are inside cells or liposomes. Generally speaking, encapsulated libraries are used to store the library members for future use; the members are extracted in some way for screening purposes. However, if they differentially affect the phenotype of the cells, they may be screened indirectly by screening the cells.

cDNA Library

A cDNA library is usually prepared by extracting RNA from cells of particular origin, fractionating the RNA to isolate the messenger RNA (mRNA has a poly(A) tail, so this is usually done by oligo-dT affinity chromatography), synthesizing complementary DNA (cDNA) using reverse transcriptase, DNA polymerase, and other enzymes, subcloning the cDNA into vectors, and introducing the vectors into cells. Often, only mRNAs or cDNAs of particular sizes will be used, to make it more likely that the cDNA encodes a functional polypeptide.

A cDNA library explores the natural diversity of the transcribed DNAs of cells from a particular source. It is not a combinatorial library.

A cDNA library may be used to make a hybridization library, or it may be used as an (or to make) expression library.

Genomic DNA Library

A genomic DNA library is made by extracting DNA from a particular source, fragmenting the DNA, isolating fragments of a particular size range, subcloning the DNA fragments into vectors, and introducing the vectors into cells.

Like a cDNA library, a genomic DNA library is a natural diversity library, and not a combinatorial library. A genomic DNA library may be used the same way as a cDNA library.

Synthetic DNA library

A synthetic DNA library may be screened directly (as a hybridization library), or used in the creation of an expression or display library of peptides/proteins.

5 Combinatorial Libraries

The term "combinatorial library" refers to a library in which the individual members are either systematic or random combinations of a limited set of basic elements, the properties of each member being dependent on the choice and
10 location of the elements incorporated into it. Typically, the members of the library are at least capable of being screened simultaneously. Randomization may be complete or partial; some positions may be randomized and others predetermined, and at random positions, the choices may be
15 limited in a predetermined manner. The members of a combinatorial library may be oligomers or polymers of some kind, in which the variation occurs through the choice of monomeric building block at one or more positions of the oligomer or polymer, and possibly in terms of the connecting
20 linkage, or the length of the oligomer or polymer, too. Or the members may be nonoligomeric molecules with a standard core structure, like the 1,4-benzodiazepine structure, with the variation being introduced by the choice of substituents at particular variable sites on the core structure. Or the
25 members may be nonoligomeric molecules assembled like a jigsaw puzzle, but wherein each piece has both one or more variable moieties (contributing to library diversity) and one or more constant moieties (providing the functionalities for coupling the piece in question to other pieces).

30 Thus, in a typical combinatorial library, chemical building blocks are at least partially randomly combined into a large number (as high as 10^{15}) of different compounds, which are then simultaneously screened for binding (or other) activity against one or more targets.

35 In a "simple combinatorial library", all of the members belong to the same class of compounds (e.g., peptides) and can be synthesized simultaneously. A "composite combinatorial library" is a mixture of two or more simple

libraries, e.g., DNAs and peptides, or peptides, peptoids, and PNAs, or benzodiazepines and carbamates. The number of component simple libraries in a composite library will, of course, normally be smaller than the average number of members in each simple library, as otherwise the advantage of a library over individual synthesis is small.

Libraries of thousands, even millions, of random oligopeptides have been prepared by chemical synthesis (Houghten et al., *Nature*, 354:84-6(1991)), or gene expression (Marks et al., *J Mol Biol*, 222:581-97(1991)), displayed on chromatographic supports (Lam et al., *Nature*, 354:82-4(1991)), inside bacterial cells (Colas et al., *Nature*, 380:548-550(1996)), on bacterial pili (Lu, *Bio/Technology*, 13:366-372(1990)), or phage (Smith, *Science*, 228:1315-7(1985)), and screened for binding to a variety of targets including antibodies (Valadon et al., *J Mol Biol*, 261:11-22(1996)), cellular proteins (Schmitz et al., *J Mol Biol*, 260:664-677(1996)), viral proteins (Hong and Boulanger, *Embo J*, 14:4714-4727(1995)), bacterial proteins (Jacobsson and Frykberg, *Biotechniques*, 18:878-885(1995)), nucleic acids (Cheng et al., *Gene*, 171:1-8(1996)), and plastic (Siani et al., *J Chem Inf Comput Sci*, 34:588-593(1994)).

Libraries of proteins (Ladner, USP 4,664,989), peptoids (Simon et al., *Proc Natl Acad Sci U S A*, 89:9367-71(1992)), nucleic acids (Ellington and Szostak, *Nature*, 246:818(1990)), carbohydrates, and small organic molecules (Eichler et al., *Med Res Rev*, 15:481-96(1995)) have also been prepared or suggested for drug screening purposes.

The first combinatorial libraries were composed of peptides or proteins, in which all or selected amino acid positions were randomized. Peptides and proteins can exhibit high and specific binding activity, and can act as catalysts. In consequence, they are of great importance in biological systems.

Nucleic acids have also been used in combinatorial libraries. Their great advantage is the ease with which a nucleic acid with appropriate binding activity can be

amplified. As a result, combinatorial libraries composed of nucleic acids can be of low redundancy and hence, of high diversity.

There has also been much interest in combinatorial libraries based on small molecules, which are more suited to pharmaceutical use, especially those which, like benzodiazepines, belong to a chemical class which has already yielded useful pharmacological agents. The techniques of combinatorial chemistry have been recognized as the most efficient means for finding small molecules that act on these targets. At present, small molecule combinatorial chemistry involves the synthesis of either pooled or discrete molecules that present varying arrays of functionality on a common scaffold. These compounds are grouped in libraries that are then screened against the target of interest either for binding or for inhibition of biological activity.

The size of a library is the number of molecules in it. The simple diversity of a library is the number of unique structures in it. There is no formal minimum or maximum diversity. If the library has a very low diversity, the library has little advantage over just synthesizing and screening the members individually. If the library is of very high diversity, it may be inconvenient to handle, at least without automatizing the process. The simple diversity of a library is preferably at least 10, 10E2, 10E3, 10E4, 10E6, 10E7, 10E8 or 10E9, the higher the better under most circumstances. The simple diversity is usually not more than 10E15, and more usually not more than 10E10.

The average sampling level is the size divided by the simple diversity. The expected average sampling level must be high enough to provide a reasonable assurance that, if a given structure were expected, as a consequence of the library design, to be present, that the actual average sampling level will be high enough so that the structure, if satisfying the screening criteria, will yield a positive result when the library is screened. Thus, the preferred average sampling level is a function of the detection limit,

which in turn is a function of the strength of the signal to be screened.

There are more complex measures of diversity than simple diversity. These attempt to take into account the degree of structural difference between the various unique sequences. These more complex measures are usually used in the context of small organic compound libraries, see below.

The library members may be presented as solutes in solution, or immobilized on some form of support. In the latter case, the support may be living (cell, virus) or nonliving (bead, plate, etc.). The supports may be separable (cells, virus particles, beads) so that binding and nonbinding members can be separated, or nonseparable (plate). In the latter case, the members will normally be placed on addressable positions on the support. The advantage of a soluble library is that there is no carrier moiety that could interfere with the binding of the members to the support. The advantage of an immobilized library is that it is easier to identify the structure of the members which were positive.

When screening a soluble library, or one with a separable support, the target is usually immobilized. When screening a library on a nonseparable support, the target will usually be labeled.

Oligonucleotide Libraries

An oligonucleotide library is a combinatorial library, at least some of whose members are single-stranded oligonucleotides having three or more nucleotides connected by phosphodiester or analogous bonds. The oligonucleotides may be linear, cyclic or branched, and may include non-nucleic acid moieties. The nucleotides are not limited to the nucleotides normally found in DNA or RNA. For examples of nucleotides modified to increase nuclease resistance and chemical stability of aptamers, see Chart 1 in Osborne and Ellington, Chem. Rev., 97: 349-70 (1997). For screening of RNA, see Ellington and Szostak, Nature, 346: 818-22 (1990).

There is no formal minimum or maximum size for these

oligonucleotides. However, the number of conformations which an oligonucleotide can assume increases exponentially with its length in bases. Hence, a longer oligonucleotide is more likely to be able to fold to adapt itself to a protein surface. On the other hand, while very long molecules can be synthesized and screened, unless they provide a much superior affinity to that of shorter molecules, they are not likely to be found in the selected population, for the reasons explained by Osborne and Ellington (1997). Hence, the libraries of the present invention are preferably composed of oligonucleotides having a length of 3 to 100 bases, more preferably 15 to 35 bases. The oligonucleotides in a given library may be of the same or of different lengths.

Oligonucleotide libraries have the advantage that libraries of very high diversity (e.g., 10^{15}) are feasible, and binding molecules are readily amplified in vitro by polymerase chain reaction (PCR). Moreover, nucleic acid molecules can have very high specificity and affinity to targets.

In a preferred embodiment, this invention prepares and screens oligonucleotide libraries by the SELEX method, as described in King and Famulok, *Molec. Biol. Repts.*, 20: 97-107 (1994); L. Gold, C. Tuerk. *Methods of producing nucleic acid ligands*, US#5595877; Oliphant et al. *Gene* 44:177 (1986).

The term "aptamer" is conferred on those oligonucleotides which bind the target protein. Such aptamers may be used to characterize the target protein, both directly (through identification of the aptamer and the points of contact between the aptamer and the protein) and indirectly (by use of the aptamer as a ligand to modify the chemical reactivity of the protein).

In a classic oligonucleotide, each nucleotide (monomeric unit) is composed of a phosphate group, a sugar moiety, and either a purine or a pyrimidine base. In DNA, the sugar is deoxyribose and in RNA it is ribose. The nucleotides are linked by 5'-3' phosphodiester bonds.

The deoxyribose phosphate backbone of DNA can be modified to increase resistance to nuclease and to increase penetration of cell membranes. Derivatives such as mono- or dithiophosphates, methyl phosphonates, boranophosphates, formacetals, carbamates, siloxanes, and dimethylenethio- -
5 sulfoxideo- and-sulfono- linked species are known in the art.

Peptide Library

10 A peptide is composed of a plurality of amino acid residues joined together by peptidyl (-NHCO-) bonds. A biogenic peptide is a peptide in which the residues are all genetically encoded amino acid residues; it is not necessary that the biogenic peptide actually be produced by gene
15 expression.

Amino acids are the basic building blocks with which peptides and proteins are constructed. Amino acids possess both an amino group (-NH₂) and a carboxylic acid group (-COOH). Many amino acids, but not all, have the alpha amino
20 acid structure NH₂-CHR-COOH, where R is hydrogen, or any of a variety of functional groups.

Twenty amino acids are genetically encoded: Alanine, Arginine, Asparagine, Aspartic Acid, Cysteine, Glutamic Acid, Glutamine, Glycine, Histidine, Isoleucine, Leucine,
25 Lysine, Methionine, Phenylalanine, Proline, Serine, Threonine, Tryptophan, Tyrosine, and Valine. Of these, all save Glycine are optically isomeric, however, only the L-form is found in humans. Nevertheless, the D-forms of these amino acids do have biological significance; D-Phe, for
30 example, is a known analgesic.

Many other amino acids are also known, including: 2-Aminoadipic acid; 3-Aminoadipic acid; beta-Aminopropionic acid; 2-Aminobutyric acid; 4-Aminobutyric acid (Piperidinic acid); 6-Aminocaproic acid; 2-Aminoheptanoic acid; 2-
35 Aminoisobutyric acid, 3-Aminoisobutyric acid; 2-Aminopimelic acid; 2,4-Diaminobutyric acid; Desmosine; 2,2'-Diaminopimelic acid; 2,3-Diaminopropionic acid; N-Ethylglycine; N-Ethylasparagine; Hydroxylysine; allo-

Hydroxylysine; 3-Hydroxyproline; 4-Hydroxyproline; Isodesmosine; allo-Isoleucine; N-Methylglycine (Sarcosine); N-Methylisoleucine; N-Methylvaline; Norvaline; Norleucine; and Ornithine.

5 Peptides are constructed by condensation of amino acids and/or smaller peptides. The amino group of one amino acid (or peptide) reacts with the carboxylic acid group of a second amino acid (or peptide) to form a peptide (-NHCO-) bond, releasing one molecule of water. Therefore, when an
10 amino acid is incorporated into a peptide, it should, technically speaking, be referred to as an amino acid residue. The core of that residue is the moiety which excludes the -NH and -CO linking functionalities which connect it to other residues. This moiety consists of one
15 or more main chain atoms (see below) and the attached side chains.

 The main chain moiety of each amino acid consists of the -NH and -CO linking functionalities and a core main chain moiety. Usually the latter is a single carbon atom.
20 However, the core main chain moiety may include additional carbon atoms, and may also include nitrogen, oxygen or sulfur atoms, which together form a single chain. In a preferred embodiment, the core main chain atoms consist solely of carbon atoms.

25 The side chains are attached to the core main chain atoms. For alpha amino acids, in which the side chain is attached to the alpha carbon, the C-1, C-2 and N-2 of each residue form the repeating unit of the main chain, and the word "side chain" refers to the C-3 and higher numbered
30 carbon atoms and their substituents. It also includes H atoms attached to the main chain atoms.

 Amino acids may be classified according to the number of carbon atoms which appear in the main chain between the carbonyl carbon and amino nitrogen atoms which participate
35 in the peptide bonds. Among the 150 or so amino acids which occur in nature, alpha, beta, gamma and delta amino acids are known. These have 1-4 intermediary carbons. Only alpha amino acids occur in proteins. Proline is a special case of

an alpha amino acid; its side chain also binds to the peptide bond nitrogen.

For beta and higher order amino acids, there is a choice as to which main chain core carbon a side chain other than H is attached to. The preferred attachment site is the C-2 (alpha) carbon, i.e., the one adjacent to the carboxyl carbon of the -CO linking functionality. It is also possible for more than one main chain atom to carry a side chain other than H. However, in a preferred embodiment, only one main chain core atom carries a side chain other than H.

A main chain carbon atom may carry either one or two side chains; one is more common. A side chain may be attached to a main chain carbon atom by a single or a double bond; the former is more common.

A simple combinatorial peptide library is one whose members are peptides having three or more amino acids connected via peptide bonds.

The peptides may be linear, branched, or cyclic, and may covalently or noncovalently include nonpeptidyl moieties. The amino acids are not limited to the naturally occurring or to the genetically encoded amino acids.

A biased peptide library is one in which one or more (but not all) residues of the peptides are constant residues.

Cyclic Peptides

Many naturally occurring peptides are cyclic. Cyclization is a common mechanism for stabilization of peptide conformation thereby achieving improved association of the peptide with its ligand and hence improved biological activity. Cyclization is usually achieved by intra-chain cystine formation, by formation of peptide bond between side chains or between N- and C- terminals. Cyclization was usually achieved by peptides in solution, but several publications have appeared that describe cyclization of peptides on beads.

A peptide library may be an oligopeptide library or a protein library.

Oligopeptides

Preferably, the oligopeptides are at least five, six, seven or eight amino acids in length. Preferably, they are composed of less than 50, more preferably less than 20 amino acids.

In the case of an oligopeptide library, all or just some of the residues may be variable. The oligopeptide may be unconstrained, or constrained to a particular conformation by, e.g., the participation of constant cysteine residues in the formation of a constraining disulfide bond.

Proteins

Proteins, like oligopeptides, are composed of a plurality of amino acids, but the term protein is usually reserved for longer peptides, which are able to fold into a stable conformation. A protein may be composed of two or more polypeptide chains, held together by covalent or noncovalent crosslinks. These may occur in a homooligomeric or a heterooligomeric state.

A peptide is considered a protein if it (1) is at least 50 amino acids long, or (2) has at least two stabilizing covalent crosslinks (e.g., disulfide bonds). Thus, conotoxins are considered proteins.

Usually, the proteins of a protein library will be characterizable as having both constant residues (the same for all proteins in the library) and variable residues (which vary from member to member). This is simply because, for a given range of variation at each position, the sequence space (simple diversity) grows exponentially with the number of residue positions, so at some point it becomes inconvenient for all residues of a peptide to be variable positions. Since proteins are usually larger than oligopeptides, it is more common for protein libraries than oligopeptide libraries to feature variable positions.

In the case of a protein library, it is desirable to focus the mutations at those sites which are tolerant of mutation. These may be determined by alanine scanning

mutagenesis or by comparison of the protein sequence to that of homologous proteins of similar activity. It is also more likely that mutation of surface residues will directly affect binding. Surface residues may be determined by inspecting a 3D structure of the protein, or by labeling the surface and then ascertaining which residues have received labels. They may also be inferred by identifying regions of high hydrophilicity within the protein.

Because proteins are often altered at some sites but not others, protein libraries can be considered a special case of the biased peptide library.

There are several reasons that one might screen a protein library instead of an oligopeptide library, including (1) a particular protein, mutated in the library, has the desired activity to some degree already, and (2) the oligopeptides are not expected to have a sufficiently high affinity or specificity since they do not have a stable conformation.

When the protein library is based on a parental protein which does not have the desired activity, the parental protein will usually be one which is of high stability (melting point ≥ 50 deg. C.) and/or possessed of hypervariable regions.

The variable domains of an antibody possess hypervariable regions and hence, in some embodiments, the protein library comprises members which comprise a mutant of VH or VL chain, or a mutant of an antigen-specific binding fragment of such a chain. VH and VL chains are usually each about 110 amino acid residues, and are held in proximity by a disulfide bond between the adjoining CL and CH1 regions to form a variable domain. Together, the VH, VL, CL and CH1 form an Fab fragment.

In human heavy chains, the hypervariable regions are at 31-35, 49-65, 98-111 and 84-88, but only the first three are involved in antigen binding. There is variation among VH and VL chains at residues outside the hypervariable regions, but to a much lesser degree.

A sequence is considered a mutant of a VH or VL chain

if it is at least 80% identical to a naturally occurring VH or VL chain at all residues outside the hypervariable region.

In a preferred embodiment, such antibody library members comprise both at least one VH chain and at least one VL chain, at least one of which is a mutant chain, and which chains may be derived from the same or different antibodies. The VH and VL chains may be covalently joined by a suitable linker moiety, as in a "single chain antibody", or they may be noncovalently joined, as in a naturally occurring variable domain.

If the joining is noncovalent, and the library is displayed on cells or virus, then either the VH or the VL chain may be fused to the carrier surface/coat protein. The complementary chain may be co-expressed, or added exogenously to the library.

The members may further comprise some or all of an antibody constant heavy and/or constant light chain, or a mutant thereof.

Peptoid Library

A peptoid is an analogue of a peptide in which one or more of the peptide bonds (-NH-CO-) are replaced by pseudopeptide bonds, which may be the same or different. It is not necessary that all of the peptide bonds be replaced, i.e., a peptoid may include one or more conventional amino acid residues, e.g., proline.

A peptide bond has two small divalent linker elements, -NH- and -CO-. Thus, a preferred class of pseudopeptide bonds are those which consist of two small divalent linker elements. Each may be chosen independently from the group consisting of amine (-NH-), substituted amine (-NR-), carbonyl (-CO-), thiocarbonyl (-CS-), methylene (-CH₂-), monosubstituted methylene (-CHR-), disubstituted methylene (-CR₁R₂-), ether (-O-) and thioether (-S-). The more preferred pseudopeptide bonds include:

N-modified -NRCO-

Carba Ψ -CH₂-CH₂-

Depsi Ψ -CO-O-
 Hydroxyethylene Ψ -CHOH-CH₂-
 Ketomethylene Ψ -CO-CH₂-
 Methylene-Oxy -CH₂-O-
 5 Reduced -CH₂-NH-
 Thiomethylene -CH₂-S-
 Thiopeptide -CS-NH-
 Retro-Inverso -CO-NH-

10 A single peptoid molecule may include more than one kind of pseudopeptide bond.

For the purposes of introducing diversity into a peptoid library, one may vary (1) the side chains attached to the core main chain atoms of the monomers linked by the pseudopeptide bonds, and/or (2) the side chains (e.g., the R of an -NRCO-) of the pseudopeptide bonds. Thus, in one embodiment, the monomeric units which are not amino acid residues are of the structure -NR₁-CR₂-CO-, where at least one of R₁ and R₂ are not hydrogen. If there is variability in the pseudopeptide bond, this is most conveniently done by using an -NRCO- or other pseudopeptide bond with an R group, and varying the R group. In this event, the R group will usually be any of the side chains characterizing the amino acids of peptides, as previously discussed.

25 If the R group of the pseudopeptide bond is not variable, it will usually be small, e.g., not more than 10 atoms (e.g., hydroxyl, amino, carboxyl, methyl, ethyl, propyl).

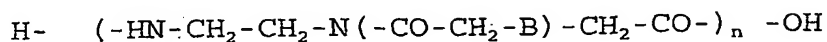
30 If the conjugation chemistries are compatible, a simple combinatorial library may include both peptides and peptoids.

Peptide Nucleic Acid Library

35 A PNA oligomer is here defined as one comprising a plurality of units, at least one of which is a PNA monomer which comprises a side chain comprising a nucleobase. For nucleobases, see USP 6,077,835.

The classic PNA oligomer is composed of (2-

aminoethyl)glycine units, with nucleobases attached by methylene carbonyl linkers. That is, it has the structure



where the outer parenthesized substructure is the PNA monomer.

In this structure, the nucleobase B is separated from the backbone N by three bonds, and the points of attachment of the side chains are separated by six bonds. The nucleobase may be any of the bases included in the nucleotides discussed in connection with oligonucleotide libraries. The bases of nucleotides A, G, T, C and U are preferred.

A PNA oligomer may further comprise one or more amino acid residues, especially glycine and proline.

One can readily envision related molecules in which (1) the -COCH₂- linker is replaced by another linker, especially one composed of two small divalent linkers as defined previously, (2) a side chain is attached to one of the three main chain carbons not participating in the peptide bond (either instead or in addition to the side chain attached to the N of the classic PNA); and/or (3) the peptide bonds are replaced by pseudopeptide bonds as disclosed previously in the context of peptoids.

PNA oligomer libraries have been made; see e.g. Cook, 6,204,326.

Small Organic Compound Library

The small organic compound library ("compound library", for short) is a combinatorial library whose members are suitable for use as drugs if, indeed, they have the ability to mediate a biological activity of the target protein.

Peptides have certain disadvantages as drugs. These include susceptibility to degradation by serum proteases, and difficulty in penetrating cell membranes. Preferably, all or most of the compounds of the compound library avoid,

or at least do not suffer to the same degree, one or more of the pharmaceutical disadvantages of peptides.

In designing a compound library, it is helpful to bear in mind the methods of molecular modification typically used to obtain new drugs. Three basic kinds of modification may be identified: disjunction, in which a lead drug is simplified to identify its component pharmacophoric moieties; conjunction, in which two or more known pharmacophoric moieties, which may be the same or different, are associated, covalently or noncovalently, to form a new drug; and alteration, in which one moiety is replaced by another which may be similar or different, but which is not in effect a disjunction or conjunction. The use of the terms "disjunction", "conjunction" and "alteration" is intended only to connote the structural relationship of the end product to the original leads, and not how the new drugs are actually synthesized, although it is possible that the two are the same.

The process of disjunction is illustrated by the evolution of neostigmine (1931) and edrophonium (1952) from physostigmine (1925). Subsequent conjunction is illustrated by demecarium (1956) and ambenonium (1956).

Alterations may modify the size, polarity, or electron distribution of an original moiety. Alterations include ring closing or opening, formation of lower or higher homologues, introduction or saturation of double bonds, introduction of optically active centers, introduction, removal or replacement of bulky groups, isosteric or bioisosteric substitution, changes in the position or orientation of a group, introduction of alkylating groups, and introduction, removal or replacement of groups with a view toward inhibiting or promoting inductive (electrostatic) or conjugative (resonance) effects.

Thus, the substituents may include electron acceptors and/or electron donors. Typical electron donors (+I) include $-\text{CH}_3$, $-\text{CH}_2\text{R}$, $-\text{CHR}_2$, $-\text{CR}_3$ and $-\text{COO}^-$. Typical electron acceptors (-I) include $-\text{NH}_3^+$, $-\text{NR}_3^+$, $-\text{NO}_2$, $-\text{CN}$, $-\text{COOH}$, $-\text{COOR}$, $-\text{CHO}$, $-\text{COR}$, $-\text{COR}$, $-\text{F}$, $-\text{Cl}$, $-\text{Br}$, $-\text{OH}$, $-\text{OR}$, $-\text{SH}$, $-\text{SR}$, $-\text{CH}=\text{CH}_2$,

-CR=CR₂, and -C=CH.

The substituents may also include those which increase or decrease electronic density in conjugated systems. The former (+R) groups include -CH₃, -CR₃, -F, -Cl, -Br, -I, -OH, 5 -OR, -OCOR, -SH, -SR, -NH₂, -NR₂, and -NHCOR. The later (-R) groups include -NO₂, -CN, -CHC, -COR, -COOH, -COOR, -CONH₂, -SO₂R and -CF₃.

Synthetically speaking, the modifications may be achieved by a variety of unit processes, including 10 nucleophilic and electrophilic substitution, reduction and oxidation, addition elimination, double bond cleavage, and cyclization.

For the purpose of constructing a library, a compound, or a family of compounds, having one or more pharmacological 15 activities (which need not be related to the known or suspected activities of the target protein), may be disjoined into two or more known or potential pharmacophoric moieties. Analogues of each of these moieties may be identified, and mixtures of these analogues reacted so as to 20 reassemble compounds which have some similarity to the original lead compound. It is not necessary that all members of the library possess moieties analogous to all of the moieties of the lead compound.

The design of a library may be illustrated by the 25 example of the benzodiazepines. Several benzodiazepine drugs, including chlordiazepoxide, diazepam and oxazepam, have been used as anti-anxiety drugs. Derivatives of benzodiazepines have widespread biological activities; derivatives have been reported to act not only as 30 anxiolytics, but also as anticonvulsants; cholecystokinin (CCK) receptor subtype A or B, kappa opioid receptor, platelet activating factor, and HIV transactivator Tat antagonists, and GPIIb/IIIa, reverse transcriptase and ras farnesyltransferase inhibitors.

35 The benzodiazepine structure has been disjoined into a 2-aminobenzophenone, an amino acid, and an alkylating agent. See Bunin, et al., Proc. Nat. Acad. Sci. USA, 91:4708 (1994). Since only a few 2-aminobenzophenone derivatives

are commercially available, it was later disjoined into 2-aminoarylstannane, an acid chloride, an amino acid, and an alkylating agent. Bunin, et al., Meth. Enzymol., 267:448 (1996). The arylstannane may be considered the core structure upon which the other moieties are substituted, or all four may be considered equals which are conjoined to make each library member.

A basic library synthesis plan and member structure is shown in Figure 1 of Fowlkes, et al., U.S. Serial No. 08/740,671, incorporated by reference in its entirety. The acid chloride building block introduces variability at the R¹ site. The R² site is introduced by the amino acid, and the R³ site by the alkylating agent. The R⁴ site is inherent in the arylstannane. Bunin, et al. generated a 1, 4-benzodiazepine library of 11,200 different derivatives prepared from 20 acid chlorides, 35 amino acids, and 16 alkylating agents. (No diversity was introduced at R⁴; this group was used to couple the molecule to a solid phase.) According to the Available Chemicals Directory (HDL Information Systems, San Leandro CA), over 300 acid chlorides, 80 Fmoc-protected amino acids and 800 alkylating agents were available for purchase (and more, of course, could be synthesized). The particular moieties used were chosen to maximize structural dispersion, while limiting the numbers to those conveniently synthesized in the wells of a microtiter plate. In choosing between structurally similar compounds, preference was given to the least substituted compound.

The variable elements included both aliphatic and aromatic groups. Among the aliphatic groups, both acyclic and cyclic (mono- or poly-) structures, substituted or not, were tested. (While all of the acyclic groups were linear, it would have been feasible to introduce a branched aliphatic). The aromatic groups featured either single and multiple rings, fused or not, substituted or not, and with heteroatoms or not. The secondary substituents included -NH₂, -OH, -OMe, -CN, -Cl, -F, and -COOH. While not used, spacer moieties, such as -O-, -S-, -OO-, -CS-, -NH-, and -

NR-, could have been incorporated.

Bunin et al. suggest that instead of using a 1, 4-benzodiazepine as a core structure, one may instead use a 1, 4-benzodiazepine-2, 5-dione structure.

5 As noted by Bunin et al., it is advantageous, although not necessary, to use a linkage strategy which leaves no trace of the linking functionality, as this permits construction of a more diverse library.

Other combinatorial nonoligomeric compound libraries
10 known or suggested in the art have been based on carbamates, mercaptoacylated pyrrolidines, phenolic agents, aminimides, N-acylamino ethers (made from amino alcohols, aromatic hydroxy acids, and carboxylic acids), N-alkylamino ethers (made from aromatic hydroxy acids, amino alcohols and
15 aldehydes) 1, 4-piperazines, and 1, 4-piperazine-6-ones.

DeWitt, et al., Proc. Nat. Acad. Sci. (USA), 90:6909-13 (1993) describe the simultaneous but separate, synthesis of 40 discrete hydantoins and 40 discrete benzodiazepines. They carry out their synthesis on a solid support (inside a
20 gas dispersion tube), in an array format, as opposed to other conventional simultaneous synthesis techniques (e.g., in a well, or on a pin). The hydantoins were synthesized by first simultaneously deprotecting and then treating each of five amino acid resins with each of eight isocyanates. The
25 benzodiazepines were synthesized by treating each of five deprotected amino acid resins with each of eight 2-amino benzophenone imines.

Chen, et al., J. Am. Chem. Soc., 116:2661-62 (1994) described the preparation of a pilot (9 member)
30 combinatorial library of formate esters. A polymer bead-bound aldehyde preparation was "split" into three aliquots, each reacted with one of three different ylide reagents. The reaction products were combined, and then divided into three new aliquots, each of which was reacted with a
35 different Michael donor. Compound identity was found to be determinable on a single bead basis by gas chromatography/mass spectroscopy analysis.

Holmes, USP 5,549,974 (1996) sets forth methodologies

for the combinatorial synthesis of libraries of thiazolidinones and metathiazanones. These libraries are made by combination of amines, carbonyl compounds, and thiols under cyclization conditions.

5 Ellman, USP 5,545,568 (1996) describes combinatorial synthesis of benzodiazepines, prostaglandins, beta-turn mimetics, and glycerol-based compounds. See also Ellman, USP 5,288,514.

10 Summerton, USP 5,506,337 (1996) discloses methods of preparing a combinatorial library formed predominantly of morpholino subunit structures.

Heterocyclic combinatorial libraries are reviewed generally in Nefzi, et al., Chem. Rev., 97:449-472 (1997).

15 For pharmacological classes, see, e.g., Goth, Medical Pharmacology: Principles and Concepts (C.V. Mosby Co.: 8th ed. 1976); Korolkovas and Burckhalter, Essentials of Medicinal Chemistry (John Wiley & Sons, Inc.: 1976). For synthetic methods, see, e.g., Warren, Organic Synthesis: The Disconnection Approach (John Wiley & Sons, Ltd.: 1982);
20 Fuson, Reactions of Organic Compounds (John Wiley & Sons: 1966); Payne and Payne, How to do an Organic Synthesis (Allyn and Bacon, Inc.: 1969); Greene, Protective Groups in Organic Synthesis (Wiley-Interscience). For selection of
25 substituents, see e.g., Hansch and Leo, Substituent Constants for Correlation Analysis in Chemistry and Biology (John Wiley & Sons: 1979).

The library is preferably synthesized so that the individual members remain identifiable so that, if a member
30 is shown to be active, it is not necessary to analyze it. Several methods of identification have been proposed, including:

- (1) encoding, i.e., the attachment to each member of an identifier moiety which is more readily
35 identified than the member proper. This has the disadvantage that the tag may itself influence the activity of the conjugate.
- (2) spatial addressing, e.g., each member is

synthesized only at a particular coordinate on or in a matrix, or in a particular chamber. This might be, for example, the location of a particular pin, or a particular well on a microtiter plate, or inside a "tea bag".

The present invention is not limited to any particular form of identification.

However, it is possible to simply characterize those members of the library which are found to be active, based on the characteristic spectroscopic indicia of the various building blocks.

Solid phase synthesis permits greater control over which derivatives are formed. However, the solid phase could interfere with activity. To overcome this problem, some or all of the molecules of each member could be liberated, after synthesis but before screening.

Examples of candidate simple libraries which might be evaluated include derivatives of the following:

Cyclic Compounds Containing One Hetero Atom

Heteronitrogen

pyrroles

pentasubstituted pyrroles

pyrrolidines

pyrrolines

prolines

indoles

beta-carbolines

pyridines

dihydropyridines

1,4-dihydropyridines

pyrido[2,3-d]pyrimidines

tetrahydro-3H-imidazo[4,5-c] pyridines

Isoquinolines

tetrahydroisoquinolines

quinolones

beta-lactams

azabicyclo[4.3.0]nonen-8-one amino acid

Heterooxygen

furans
tetrahydrofurans
2,5-disubstituted tetrahydrofurans
pyrans
5 hydroxypyranones
tetrahydroxypyranones
gamma-butyrolactones
Heterosulfur
sulfolenes
10 Cyclic Compounds with Two or More Hetero atoms
Multiple heteronitrogens
imidazoles
pyrazoles
piperazines
15 diketopiperazines
arylpiperazines
benzylpiperazines
benzodiazepines
1,4-benzodiazepine-2,5-diones
20 hydantoins
5-alkoxyhydantoins
dihydropyrimidines
1,3-disubstituted-5,6-dihydropyrimidine-2,4-
25 diones
cyclic ureas
cyclic thioureas
quinazolines
chiral 3-substituted-quinazoline-2,4-
30 diones
triazoles
1,2,3-triazoles
purines
Heteronitrogen and Heterooxygen
35 dikelomorpholines
isoxazoles
isoxazolines
Heteronitrogen and Heterosulfur

thiazolidines

N-axylthiazolidines

dihydrothiazoles

2-methylene-2,3-dihydrothiazates

2-aminothiazoles

thiophenes

3-amino thiophenes

4-thiazolidinones

4-melathiazanones

benzisothiazolones

For details on synthesis of libraries, see Nefzi, et al., Chem. Rev., 97:449-72 (1997), and references cited therein.

Pharmaceutical Methods and Preparations

The preferred animal subject of the present invention is a mammal. By the term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects, although it is intended for veterinary and nutritional uses as well. Preferred nonhuman subjects are of the orders Primata (e.g., apes and monkeys), Artiodactyla or Perissodactyla (e.g., cows, pigs, sheep, horses, goats), Carnivora (e.g., cats, dogs), Rodenta (e.g., rats, mice, guinea pigs, hamsters), Lagomorpha (e.g., rabbits) or other pet, farm or laboratory mammals.

The term "protection", as used herein, is intended to include "prevention," "suppression" and "treatment." "Prevention", strictly speaking, involves administration of the pharmaceutical prior to the induction of the disease (or other adverse clinical condition). "Suppression" involves administration of the composition prior to the clinical appearance of the disease. "Treatment" involves administration of the protective composition after the appearance of the disease.

It will be understood that in human and veterinary medicine, it is not always possible to distinguish between "preventing" and "suppressing" since the ultimate inductive

event or events may be unknown, latent, or the patient is not ascertained until well after the occurrence of the event or events. Therefore, unless qualified, the term "prevention" will be understood to refer to both prevention in the strict sense, and to suppression.

The preventative or prophylactic use of a pharmaceutical involves identifying subjects who are at higher risk than the general population of contracting the disease, and administering the pharmaceutical to them in advance of the clinical appearance of the disease. The effectiveness of such use is measured by comparing the subsequent incidence or severity of the disease, or of particular symptoms of the disease, in the treated subjects against that in untreated subjects of the same high risk group.

While high risk factors vary from disease to disease, in general, these include (1) prior occurrence of the disease in one or more members of the same family, or, in the case of a contagious disease, in individuals with whom the subject has come into potentially contagious contact at a time when the earlier victim was likely to be contagious, (2) a prior occurrence of the disease in the subject, (3) prior occurrence of a related disease, or a condition known to increase the likelihood of the disease, in the subject; (4) appearance of a suspicious level of a marker of the disease, or a related disease or condition; (5) a subject who is immunologically compromised, e.g., by radiation treatment, HIV infection, drug use,, etc., or (6) membership in a particular group (e.g., a particular age, sex, race, ethnic group, etc.) which has been epidemiologically associated with that disease.

A prophylaxis or treatment may be curative, that is, directed at the underlying cause of a disease, or ameliorative, that is, directed at the symptoms of the disease, especially those which reduce the quality of life.

It should also be understood that to be useful, the protection provided need not be absolute, provided that it is sufficient to carry clinical value. An agent which

provides protection to a lesser degree than do competitive agents may still be of value if the other agents are ineffective for a particular individual, if it can be used in combination with other agents to enhance the level of protection, or if it is safer than competitive agents. It is desirable that there be a statistically significant ($p=0.05$ or less) improvement in the treated subject relative to an appropriate untreated control, and it is desirable that this improvement be at least 10%, more preferably at least 25%, still more preferably at least 50%, even more preferably at least 100%, in some indicia of the incidence or severity of the disease or of at least one symptom of the disease.

At least one of the drugs of the present invention may be administered, by any means that achieve their intended purpose, to protect a subject against a disease or other adverse condition. The form of administration may be systemic or topical. For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. Parenteral administration can be by bolus injection or by gradual perfusion over time.

A typical regimen comprises administration of an effective amount of the drug, administered over a period ranging from a single dose, to dosing over a period of hours, days, weeks, months, or years.

It is understood that the suitable dosage of a drug of the present invention will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired. However, the most preferred dosage can be tailored to the individual subject, as is understood and determinable by one of skill in the art, without undue experimentation. This will typically involve adjustment of a standard dose, e.g., reduction of the dose if the patient has a low body weight.

Prior to use in humans, a drug will first be evaluated

for safety and efficacy in laboratory animals. In human clinical studies, one would begin with a dose expected to be safe in humans, based on the preclinical data for the drug in question, and on customary doses for analogous drugs (if any). If this dose is effective, the dosage may be decreased, to determine the minimum effective dose, if desired. If this dose is ineffective, it will be cautiously increased, with the patients monitored for signs of side effects. See, e.g., Berkow et al, eds., *The Merck Manual*, 15th edition, Merck and Co., Rahway, N.J., 1987; Goodman et al., eds., *Goodman and Gilman's The Pharmacological Basis of Therapeutics*, 8th edition, Pergamon Press, Inc., Elmsford, N.Y., (1990); Avery's *Drug Treatment: Principles and Practice of Clinical Pharmacology and Therapeutics*, 3rd edition, ADIS Press, LTD., Williams and Wilkins, Baltimore, MD. (1987), Ebadi, *Pharmacology*, Little, Brown and Co., Boston, (1985), which references and references cited therein, are entirely incorporated herein by reference.

The total dose required for each treatment may be administered by multiple doses or in a single dose. The protein may be administered alone or in conjunction with other therapeutics directed to the disease or directed to other symptoms thereof.

Typical pharmaceutical doses, for adult humans, are in the range of 1 ng to 10g per day, more often 1 mg to 1g per day.

The appropriate dosage form will depend on the disease, the pharmaceutical, and the mode of administration; possibilities include tablets, capsules, lozenges, dental pastes, suppositories, inhalants, solutions, ointments and parenteral depots. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, including all references cited therein.

In the case of peptide drugs, the drug may be administered in the form of an expression vector comprising a nucleic acid encoding the peptide; such a vector, after incorporation into the genetic complement of a cell of the

patient, directs synthesis of the peptide. Suitable vectors include genetically engineered poxviruses (vaccinia), adenoviruses, adeno-associated viruses, herpesviruses and lentiviruses which are or have been rendered nonpathogenic.

5 In addition to at least one drug as described herein, a pharmaceutical composition may contain suitable pharmaceutically acceptable carriers, such as excipients, carriers and/or auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. See, e.g., Berker, *supra*, Goodman, *supra*, Avery, *supra* and Ebadi, *supra*, which are entirely incorporated herein by reference, included all references cited therein.

15 Assay Compositions and Methods

Target Organism

The invention contemplates that it may be appropriate to ascertain or to mediate the biological activity of a substance of this invention in a target organism.

20 The target organism may be a plant, animal, or microorganism.

In the case of a plant, it may be an economic plant, in which case the drug may be intended to increase the disease, weather or pest resistance, alter the growth characteristics, or otherwise improve the useful characteristics or mute undesirable characteristics of the plant. Or it may be a weed, in which case the drug may be intended to kill or otherwise inhibit the growth of the plant, or to alter its characteristics to convert it from a weed to an economic plant. The plant may be a tree, shrub, crop, grass, etc. The plant may be an algae (which are in some cases also microorganisms), or a vascular plant, especially gymnosperms (particularly conifers) and angiosperms. Angiosperms may be monocots or dicots. The plants of greatest interest are rice, wheat, corn, alfalfa, soybeans, potatoes, peanuts, tomatoes, melons, apples, pears, plums, pineapples, fir, spruce, pine, cedar, and oak.

If the target organism is a microorganism, it may be

electrodes in the chip were used to create electrokinetic forces capable of driving molecules through these micro-channels to perform electrophoretic separations. Ribosomal peaks were measured by fluorescence signal and displayed in an electropherogram. A successful total RNA sample featured 2 distinct ribosomal peaks (18S and 28S rRNA).

Biotinylated cRNA Hybridization Target.

Total RNA was prepared for use as a hybridization target as described in the manufacturer's instructions for CodeLink Expression Bioarrays(TM) (Amersham Biosciences). The CodeLink Expression Bioarrays utilize nucleic acid hybridization of a biotin-labeled complementary RNA(cRNA) target with DNA oligonucleotide probes attached to a gel matrix.

The biotin-labeled cRNA target is prepared by a linear amplification method. Poly (A) + RNA (within the total RNA population) is primed for reverse transcription by a DNA oligonucleotide containing a T7 RNA polymerase promoter 5' to a (dT) 24 sequence. After second-strand cDNA synthesis, the cDNA serves as the template in an *in vitro* transcription (IVT) reaction to produce the target cRNA. The IVT is performed in the presence of biotinylated nucleotides to label the target cRNA. This procedure results in a 50-200 fold linear amplification of the input poly (A) + RNA.

Hybridization Probes.

The oligonucleotide probes were provided by the Codelink Uniset Mouse I Bioarray (Amersham, product code 300013). Amine-terminated oligonucleotide probes are attached to a three-dimensional polyacrylamide gel matrix. There are 10,000 oligonucleotide probes, each specific to a well-characterized mouse gene. Each mouse gene is representative of a unique gene cluster from the fourth quarter 2001 Genbank Unigene build. There are also 500 control probes.

The sequences of the probes is proprietary to Amersham. However, for each probe, Amersham identifies the

corresponding mouse gene by NCBI accession number, OGS, LocusLink, Unigene Cluster ID, and description (name). This information should be available from Amersham. In the case of the differentially expressed probes, this information is duplicated in master table 1. For the complete list, see http://www4.amershambiosciences.com/aptrix/upp01077.nsf/Content/codelink_literature

Under "Gene Lists", select "Uniset Human I", and a gene list, in Excel format, can be downloaded.

Hybridization

Using the cRNA target, the hybridization reaction mixture is prepared and loaded until array chambers for bioarray processing as set forth in the manufacturer's instructions for CodeLink Gene Expression Bioarrays™ (Amersham Biosciences). Each sample is hybridized to an individual microarray. Hybridization is at 37°C. The hybridization buffer is prepared as set forth in the Motorola instructions. Hybridization to the microarray is detected with an avidinated fluorescent reagent, Streptavidin-Alexa Fluor® 647 (Amersham).

Mouse Gene Expression Analysis

Processed arrays were scanned using a GenePix 4000B Microarray Scanner (Axon Instruments, Inc.); array images were acquired using the Amersham CodeLink™ Analysis Software (Release 2.2). The Amersham CodeLink™ Analysis Software gives an integrated optical density (IOD) value for every spot; a unique background value for that spot is subtracted, resulting in "raw" data points. Individual chips are then normalized by the Amersham CodeLink™ software according to the median raw intensity for all 10,000 genes. A negative control threshold is also calculated according to the control probes. A significant difference in expression between samples was defined as a minimum of 2-fold change in expression values. Genes with expression values below the

negative control threshold were eliminated from the analysis and then the expression data was analyzed to identify genes whose expression levels changed significantly with respect to:

5 Normal mice compared to hyperinsulinemic mice at 2, 4, 8 and 16 weeks, and 6 months, on normal vs. high-fat diet.

10 Normal mice compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 weeks, and 6 months, on normal vs. high-fat diet.

15 Hyperinsulinemic compared to hyperinsulinemic/hyperglycemic mice at 2, 4, 8 and 16 weeks, and 6 months, on high-fat diets.

Database Searches Nucleotide sequences and predicted amino acid sequences were compared to public domain databases using the Blast 2.0 program (National Center for Biotechnology Information, National Institutes of Health). Nucleotide sequences were displayed using ABI prism Edit View 1.0.1 (PE Applied Biosystems, Foster City, CA).

20 Nucleotide database searches were conducted with the then current version of BLASTN 2.0.12, see Altschul, et al., "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res., 25:3389-3402 (1997). Searches employed the default parameters, unless otherwise stated.

30 For blastN searches, the default was the blastN matrix (1,-3), with gap penalties of 5 for existence and 2 for extension.

35 Protein database searches were conducted with the then-current version of BLAST X, see Altschul et al. (1997), supra. Searches employed the default parameters, unless otherwise stated. The scoring matrix was BLOSUM62, with gap costs of 11 for existence and 1 for extension. The standard low complexity filter was used.

"ref" indicates that NCBI's RefSeq is the source database. The identifier that follows is a RefSeq accession number, not a GenBank accession number. "RefSeq sequences are derived from GenBank and provide non-redundant curated data representing our current knowledge of known genes. Some records include additional sequence information that was never submitted to an archival database but is available in the literature. A small number of sequences are provided through collaboration; the underlying primary sequence data is available in GenBank, but may not be available in any one GenBank record. RefSeq sequences are not submitted primary sequences. RefSeq records are owned by NCBI and therefore can be updated as needed to maintain current annotation or to incorporate additional sequence information." See also <http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>

It will be appreciated by those in the art that the exact results of a database search will change from day to day, as new sequences are added. Also, if you query with a longer version of the original sequence, the results will change. The results given here were obtained at one time and no guarantee is made that the exact same hits would be obtained in a search on the filing date. However, if an alignment between a particular query sequence and a particular database sequence is discussed, that alignment should not change (if the parameters and sequences remain unchanged).

Northern Analysis.

Northern analysis may be used to confirm the results. Favorable and unfavorable genes, identified as described above, or fragments thereof, will be used as probes in Northern hybridization analyses to confirm their differential expression. Total RNA isolated from Control, Hyperinsulinemic and Type-II Diabetic mice will be resolved by agarose gel electrophoresis through a 1% agarose, 1 % formaldehyde denaturing gel, transferred to positively charged nylon membrane, and hybridized to a probe labeled

with [32P] dCTP that was generated from the aforementioned gene or fragment using the Random Primed DNA Labeling Kit (Roche, Palo Alto, CA).

5 Real-Time RNA Analysis.

Real-time RNA analysis may also be used for confirmation. For "real-time" RNA analysis, RNA will be converted to cDNA and then probed with gene-specific primers made for each clone. "Real-time" incorporation of
10 fluorescent dye will be measured to determine the amount of specific transcript present in each sample. Sample differences (control vs. hyperinsulinemic, hyperinsulinemic vs. diabetic, or control vs. diabetic) of 2-fold or greater (in either direction) will be considered differentially
15 expressed. Confirmation using several independent animals is desirable.

In situ Hybridization

Another form of confirmation may be provided by
20 nonisotopic *in situ* hybridizations (NISH) on selected human (obtained by Tissue Informatics) and mouse tissues using cRNA probes generated from mouse genes found to be up- or down-regulated during the disease progression. Nonisotopic
in situ hybridizations may also be performed on mouse
25 tissues using cRNA probes generated from all "novel" cDNA's identified through PCR subtractive hybridizations. These cRNA's will hybridize to their corresponding messenger RNA's present in cells and will provide information regarding the particular cell types within a tissue that is expressing the
30 particular gene as well as the relative level of gene expression. The cRNA probes may be generated by *in vitro* transcription of template cDNA by Sp6 or T7 RNA polymerase in the presence of digoxigenin-11-UTP (Roche Molecular Biochemicals, Mannheim, Germany; Pardue, M.L. 1985. In: *In situ*
35 *in situ* hybridization, Nucleic acid hybridization, a practical approach: IRL Press, Oxford, 179-202).

Transgenic Animals.

Transgenic expression may be used to confirm the results. In one embodiment, a mouse is engineered to overexpress the favorable or unfavorable mouse gene in question. In another embodiment, a mouse is engineered to express the
5 corresponding favorable or unfavorable human gene. In a third embodiment, a nonhuman animal other than a mouse, such as a rat, rabbit, goat, sheep or pig, is engineered to express the favorable or unfavorable mouse or human gene.

10 Hyperquantitative Tissue Analysis

In addition to gene expression analysis the liver sections can also be analyzed using TissueInformatics, Inc's TissueAnalytics™ software. A single representative section may be cut from each liver block, placed on a slide, and
15 stained with H&E. Digital images of each slide may be acquired using an research microscope and digital camera (Olympus E600 microscope and Sony DKC-ST5). These images were acquired at 20x magnification with a resolution of 0.64 mm/pixel. A hyperquantitative analysis may be performed on
20 the resulting images: First a digital image analysis can identify and annotate structural objects in a tissue using machine vision. These objects, that are constituents of the tissue, can be annotated because they are visually identifiable and have a biological meaning like hepatocytes,
25 sinusoids, vacuoles. Subsequently a quantification of these structures regarding their geometric properties like area or stain intensities and their relationship to the field of view or per unit area in terms of a % coverage may be performed. Features or parameters for hyper-quantification
30 are specific for each tissue, and may also include relations between features, measures of overall heterogeneity, including orientation, relative locations, and textures.

Correlation Analysis

35 Mathematical statistics provides a rich set of additional tools to analyze time resolved data sets of hyper-quantitative and gene expression profiles for similarities, including rank correlation, the calculation of regression

and correlations coefficients, and clustering. Continuous functions may also be fitted through the data points of individual gene and tissue feature data. Relation between gene expression and hyper-quantitative tissue data may be linear or non-linear, in synchronous or asynchronous arrangements.

A Spearman rank correlation analysis using was done on the 2 classes of measurements (Genes and Tissues Features) to help identify other significant genes. A small number of genes that did not meet the 2-Fold difference for significance were added to the list of genes based on their correlation with tissue features.

Citation of documents herein is not intended as an admission that any of the documents cited herein is pertinent prior art, or an admission that the cited documents is considered material to the patentability of any of the claims of the present application. All statements as to the date or representation as to the contents of these documents is based on the information available to the applicant and does not constitute any admission as to the correctness of the dates or contents of these documents.

The appended claims are to be treated as a non-limiting recitation of preferred embodiments.

In addition to those set forth elsewhere, the following references are hereby incorporated by reference, in their most recent editions as of the time of filing of this application: Kay, Phage Display of Peptides and Proteins: A Laboratory Manual; the John Wiley and Sons Current Protocols series, including Ausubel, Current Protocols in Molecular Biology; Coligan, Current Protocols in Protein Science; Coligan, Current Protocols in Immunology; Current Protocols in Human Genetics; Current Protocols in Cytometry; Current Protocols in Pharmacology; Current Protocols in Neuroscience; Current Protocols in Cell Biology; Current Protocols in Toxicology; Current Protocols in Field Analytical Chemistry; Current Protocols in Nucleic Acid Chemistry; and Current Protocols in Human Genetics; and the following Cold Spring Harbor Laboratory publications: Sambrook, Molecular Cloning: A Laboratory Manual; Harlow, Antibodies: A Laboratory Manual; Manipulating the Mouse Embryo: A Laboratory Manual; Methods in Yeast Genetics: A Cold Spring Harbor Laboratory Course Manual; Drosophila Protocols; Imaging Neurons: A Laboratory Manual; Early Development of *Xenopus laevis*: A Laboratory Manual; Using Antibodies: A Laboratory Manual; At the Bench: A Laboratory Navigator; Cells: A Laboratory Manual; Methods in Yeast Genetics: A Laboratory Course Manual; Discovering Neurons: The Experimental Basis of Neuroscience; Genome Analysis: A Laboratory Manual Series ; Laboratory DNA Science; Strategies for Protein Purification and Characterization: A

Laboratory Course Manual; Genetic Analysis of Pathogenic Bacteria: A Laboratory Manual; PCR Primer: A Laboratory Manual; Methods in Plant Molecular Biology: A Laboratory Course Manual ; Manipulating the Mouse Embryo: A Laboratory Manual; Molecular Probes of the Nervous System; Experiments with Fission Yeast: A Laboratory Course Manual; A Short Course in Bacterial Genetics: A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria; DNA Science: A First Course in Recombinant DNA Technology; Methods in Yeast Genetics: A Laboratory Course Manual; Molecular Biology of Plants: A Laboratory Course Manual.

All references cited herein, including journal articles or abstracts, published, corresponding, prior or otherwise related U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology

or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

5 Any description of a class or range as being useful or preferred in the practice of the invention shall be deemed a description of any subclass (e.g., a disclosed class with one or more disclosed members omitted) or subrange contained therein, as well as a separate description of each
10 individual member or value in said class or range.

The description of preferred embodiments individually shall be deemed a description of any possible combination of such preferred embodiments, except for combinations which are impossible (e.g, mutually exclusive choices for an
15 element of the invention) or which are expressly excluded by this specification.

If an embodiment of this invention is disclosed in the prior art, the description of the invention shall be deemed to include the invention as herein disclosed with such
20 embodiment excised.

Introduction to Master Tables

The master tables reflect applicants' analysis of the gene chip data.

5

For each probe corresponding to a differentially expressed mouse gene, Master Table 1 identifies

10

Col. 1: The mouse gene (upper) and mouse protein (lower) database accession #s.

Col. 2: The corresponding mouse Unigene Cluster, as of the 4th Quarter 2001 build.

15

Col. 3: The behavior (differential expression) observed for the mouse gene. This column identifies the gene as favorable(F) or unfavorable (U) on the basis of its differential behavior. There are three possible comparisons, HI-D, C-HI, and C-D, where C=control (normal), HI=hyperinsulinemic, and D=diabetic.

20

If the level of the gene in the former state is at least two-fold that in the latter state, it is considered unfavorable. If the level of the gene in the former state is not more than half (i.e., not more than negative two fold) that in the latter state, it is considered favorable.

25

Col. 4: A related human protein, identified by its database accession number. Usually, several such proteins are identified relative to each mouse gene. These proteins have been identified by BLAST searches, as explained in cols. 6-8.

30

Col. 5: The name of the related human protein.

35

Col. 6: The score (in bits) for the alignment performed by the BLAST program.

Col. 7: The E-value for the alignment performed by the BLAST program. It is worth noting that Unigene considers a Blastx E Value of less than $1e-6$ to be a "match" to the reference sequence of a cluster.

Col. 8: The BLAST search strategy used. MG indicates that the mouse gene was used as the query sequence in a BlastX search. MP means that the mouse protein was used as the query sequence in a BlastP search. HGP means that first the mouse gene was used in a BlastN search for a human gene, and then the human gene was used in a BLASTX search for the human protein.

Master Table 1 is divided into three subtables on the basis of the Behavior" in col. 3. If a gene has at least one favorable behavior, and no unfavorable ones, it is put into Subtable 1A. In the opposite case, it is put into Subtable 1B. If its behavior is mixed, i.e., at least one favorable and at least one unfavorable, it is put into Subtable 1C.

Master Table 2 has just three columns.

Col. 1: Mouse gene.

Col. 2: behavior. Same as col. 3 in Master table 1.

Col. 3: Human protein classes. Based on the related human proteins defined in Master Table 1, Master Table 2 generalizes, if possible as to classes of human proteins which are expected to have similar behavior. For a given mouse gene, several human protein classes may be listed because of the diversity of the human proteins found to be related. In some cases, the stated human protein classes may be hierarchial, e.g., one may be a subset of another. In other cases, the stated classes may be non-overlapping but related. And in yet other cases, the stated classes may be

algae, bacteria, fungi, or a virus (although the biological activity of a virus must be determined in a virus-infected cell). The microorganism may be human or other animal or plant pathogen, or it may be nonpathogenic. It may be a soil or water organism, or one which normally lives inside other living things.

If the target organism is an animal, it may be a vertebrate or a nonvertebrate animal. Nonvertebrate animals are chiefly of interest when they act as pathogens or parasites, and the drugs are intended to act as biocidal or biostatic agents. Nonvertebrate animals of interest include worms, mollusks, and arthropods.

The target organism may also be a vertebrate animal, i.e., a mammal, bird, reptile, fish or amphibian. Among mammals, the target animal preferably belongs to the order Primata (humans, apes and monkeys), Artiodactyla (e.g., cows, pigs, sheep, goats, horses), Rodenta (e.g., mice, rats), Lagomorpha (e.g., rabbits, hares), or Carnivora (e.g., cats, dogs). Among birds, the target animals are preferably of the orders Anseriformes (e.g., ducks, geese, swans) or Galliformes (e.g., quails, grouse, pheasants, turkeys and chickens). Among fish, the target animal is preferably of the order Clupeiformes (e.g., sardines, shad, anchovies, whitefish, salmon).

Target Tissues

The term "target tissue" refers to any whole animal, physiological system, whole organ, part of organ, miscellaneous tissue, cell, or cell component (e.g., the cell membrane) of a target animal in which biological activity may be measured.

Routinely in mammals one would choose to compare and contrast the biological impact on virtually any and all tissues which express the subject receptor protein. The main tissues to use are: brain, heart, lung, kidney, liver, pancreas, skin, intestines, adipose, stomach, skeletal muscle, adrenal glands, breast, prostate, vasculature, retina, cornea, thyroid gland, parathyroid glands, thymus,

bone marrow, bone, etc.

Another classification would be by cell type: B cells, T cells, macrophages, neutrophils, eosinophils, mast cells, platelets, megakaryocytes, erythrocytes, bone marrow stomal
5 cells, fibroblasts, neurons, astrocytes, neuroglia, microglia, epithelial cells (from any organ, e.g. skin, breast, prostate, lung, intestines etc), cardiac muscle cells, smooth muscle cells, striated muscle cells, osteoblasts, osteocytes, chondroblasts, chondrocytes,
10 keratinocytes, melanocytes, etc.

Of course, in the case of a unicellular organism, there is no distinction between the "target organism" and the "target tissue".

15 Screening Assays

Assays intended to determine the binding or the biological activity of a substance are called preliminary screening assays.

Screening assays will typically be either in vitro
20 (cell-free) assays (for binding to an immobilized receptor) or cell-based assays (for alterations in the phenotype of the cell). They will not involve screening of whole multicellular organisms, or isolated organs. The comments on diagnostic biological assays apply mutatis mutandis to
25 screening cell-based assays.

In Vitro vs. In Vivo Assays

The term *in vivo* is descriptive of an event, such as binding or enzymatic action, which occurs within a living
30 organism. The organism in question may, however, be genetically modified. The term *in vitro* refers to an event which occurs outside a living organism. Parts of an organism (e.g., a membrane, or an isolated biochemical) are used, together with artificial substrates and/or conditions.
35 For the purpose of the present invention, the term *in vitro* excludes events occurring inside or on an intact cell, whether of a unicellular or multicellular organism.

In vivo assays include both cell-based assays, and

organismic assays. The cell-based assays include both assays on unicellular organisms, and assays on isolated cells or cell cultures derived from multicellular organisms. The cell cultures may be mixed, provided that they are not organized into tissues or organs. The term organismic assay refers to assays on whole multicellular organisms, and assays on isolated organs or tissues of such organisms.

In vitro Diagnostic Methods and Reagents

The in vitro assays of the present invention may be applied to any suitable analyte-containing sample, and may be qualitative or quantitative in nature.

Sample

The sample will normally be a biological fluid, such as blood, urine, lymph, semen, milk, or cerebrospinal fluid, or a fraction or derivative thereof, or a biological tissue, in the form of, e.g., a tissue section or homogenate. However, the sample conceivably could be (or derived from) a food or beverage, a pharmaceutical or diagnostic composition, soil, or surface or ground water. If a biological fluid or tissue, it may be taken from a human or other mammal, vertebrate or animal, or from a plant. The preferred sample is blood, or a fraction or derivative thereof.

Binding and Reaction Assays

The assay may be a binding assay, in which one step involves the binding of a diagnostic reagent to the analyte, or a reaction assay, which involves the reaction of a reagent with the analyte. The reagents used in a binding assay may be classified as to the nature of their interaction with analyte: (1) analyte analogues, or (2) analyte binding molecules (ABM). They may be labeled or insolubilized.

In a reaction assay, the assay may look for a direct reaction between the analyte and a reagent which is reactive with the analyte, or if the analyte is an enzyme or enzyme

inhibitor, for a reaction catalyzed or inhibited by the analyte. The reagent may be a reactant, a catalyst, or an inhibitor for the reaction.

5 An assay may involve a cascade of steps in which the product of one step acts as the target for the next step. These steps may be binding steps, reaction steps, or a combination thereof.

Signal Producing System (SPS)

10 In order to detect the presence, or measure the amount, of an analyte, the assay must provide for a signal producing system (SPS) in which there is a detectable difference in the signal produced, depending on whether the analyte is
15 present or absent (or, in a quantitative assay, on the amount of the analyte). The detectable signal may be one which is visually detectable, or one detectable only with instruments. Possible signals include production of colored or luminescent products, alteration of the characteristics
20 (including amplitude or polarization) of absorption or emission of radiation by an assay component or product, and precipitation or agglutination of a component or product. The term "signal" is intended to include the discontinuance of an existing signal, or a change in the rate of change of
25 an observable parameter, rather than a change in its absolute value. The signal may be monitored manually or automatically.

In a reaction assay, the signal is often a product of the reaction. In a binding assay, it is normally provided
30 by a label borne by a labeled reagent.

Labels

The component of the signal producing system which is most intimately associated with the diagnostic reagent is
35 called the "label". A label may be, e.g., a radioisotope, a fluorophore, an enzyme, a co-enzyme, an enzyme substrate, an electron-dense compound, an agglutinable particle.

The radioactive isotope can be detected by such means

as the use of a gamma counter or a scintillation counter or by autoradiography. Isotopes which are particularly useful for the purpose of the present invention include ^3H , ^{125}I , ^{131}I , ^{35}S , ^{14}C , ^{32}P and ^{33}P . ^{125}I is preferred for antibody
5 labeling.

The label may also be a fluorophore. When the fluorescently labeled reagent is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent
10 labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthalaldehyde and fluorescamine.

Alternatively, fluorescence-emitting metals such as ^{125}Eu , or others of the lanthanide series, may be
15 incorporated into a diagnostic reagent using such metal chelating groups as diethylenetriaminepentaacetic acid (DTPA) or ethylenediamine-tetraacetic acid (EDTA).

The label may also be a chemiluminescent compound. The presence of the chemiluminescently labeled reagent is then
20 determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isolumino, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used for
25 labeling. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by
30 detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Enzyme labels, such as horseradish peroxidase and alkaline phosphatase, are preferred. When an enzyme label
35 is used, the signal producing system must also include a substrate for the enzyme. If the enzymatic reaction product is not itself detectable, the SPS will include one or more additional reactants so that a detectable product appears.

An enzyme analyte may act as its own label if an enzyme inhibitor is used as a diagnostic reagent.

Binding Assay Formats

5 Binding assays may be divided into two basic types, heterogeneous and homogeneous. In heterogeneous assays, the interaction between the affinity molecule and the analyte does not affect the label, hence, to determine the amount or presence of analyte, bound label must be separated from free
10 label. In homogeneous assays, the interaction does affect the activity of the label, and therefore analyte levels can be deduced without the need for a separation step.

In one embodiment, the ABM is insolubilized by coupling it to a macromolecular support, and analyte in the sample is
15 allowed to compete with a known quantity of a labeled or specifically labelable analyte analogue. The "analyte analogue" is a molecule capable of competing with analyte for binding to the ABM, and the term is intended to include analyte itself. It may be labeled already, or it may be
20 labeled subsequently by specifically binding the label to a moiety differentiating the analyte analogue from analyte. The solid and liquid phases are separated, and the labeled analyte analogue in one phase is quantified. The higher the level of analyte analogue in the solid phase, i.e.,
25 sticking to the ABM, the lower the level of analyte in the sample.

In a "sandwich assay", both an insolubilized ABM, and a labeled ABM are employed. The analyte is captured by the insolubilized ABM and is tagged by the labeled ABM, forming
30 a ternary complex. The reagents may be added to the sample in either order, or simultaneously. The ABMs may be the same or different. The amount of labeled ABM in the ternary complex is directly proportional to the amount of analyte in the sample.

35 The two embodiments described above are both heterogeneous assays. However, homogeneous assays are conceivable. The key is that the label be affected by whether or not the complex is formed.

Conjugation Methods

A label may be conjugated, directly or indirectly (e.g., through a labeled anti-ABM antibody), covalently (e.g., with SPDP) or noncovalently, to the ABM, to produce a
5 diagnostic reagent. Similarly, the ABM may be conjugated to a solid phase support to form a solid phase ("capture") diagnostic reagent.

Suitable supports include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases,
10 natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention.

The support material may have virtually any possible
15 structural configuration so long as the coupled molecule is capable of binding to its target. Thus the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may
20 be flat such as a sheet, test strip, etc.

Biological Assays

A biological assay measures or detects a biological response of a biological entity to a substance.

25 The biological entity may be a whole organism, an isolated organ or tissue, freshly isolated cells, an immortalized cell line, or a subcellular component (such as a membrane; this term should not be construed as including an isolated receptor). The entity may be, or may be derived
30 from, an organism which occurs in nature, or which is modified in some way. Modifications may be genetic (including radiation and chemical mutants, and genetic engineering) or somatic (e.g., surgical, chemical, etc.). In the case of a multicellular entity, the modifications may
35 affect some or all cells. The entity need not be the target organism, or a derivative thereof, if there is a reasonable correlation between bioassay activity in the assay entity and biological activity in the target organism.

The entity is placed in a particular environment, which may be more or less natural. For example, a culture medium may, but need not, contain serum or serum substitutes, and it may, but need not, include a support matrix of some kind, it may be still, or agitated. It may contain particular biological or chemical agents, or have particular physical parameters (e.g., temperature), that are intended to nourish or challenge the biological entity.

There must also be a detectable biological marker for the response. At the cellular level, the most common markers are cell survival and proliferation, cell behavior (clustering, motility), cell morphology (shape, color), and biochemical activity (overall DNA synthesis, overall protein synthesis, and specific metabolic activities, such as utilization of particular nutrients, e.g., consumption of oxygen, production of CO₂, production of organic acids, uptake or discharge of ions).

The direct signal produced by the biological marker may be transformed by a signal producing system into a different signal which is more observable, for example, a fluorescent or colorimetric signal.

The entity, environment, marker and signal producing system are chosen to achieve a clinically acceptable level of sensitivity, specificity and accuracy.

In some cases, the goal will be to identify substances which mediate the biological activity of a natural biological entity, and the assay is carried out directly with that entity. In other cases, the biological entity is used simply as a model of some more complex (or otherwise inconvenient to work with) biological entity. In that event, the model biological entity is used because activity in the model system is considered more predictive of activity in the ultimate natural biological entity than is simple binding activity in an in vitro system. The model entity is used instead of the ultimate entity because the former is more expensive or slower to work with, or because ethical considerations forbid working with the ultimate entity yet.

The model entity may be naturally occurring, if the model entity usefully models the ultimate entity under some conditions. Or it may be non-naturally occurring, with modifications that increase its resemblance to the ultimate entity.

Transgenic animals, such as transgenic mice, rats, and rabbits, have been found useful as model systems.

In cell-based model assays, where the biological activity is mediated by binding to a receptor (target protein), the receptor may be functionally connected to a signal (biological marker) producing system, which may be endogenous or exogenous to the cell. There are a number of techniques of doing this.

"Zero-Hybrid" Systems

In these systems, the binding of a peptide to the target protein results in a screenable or selectable phenotypic change, without resort to fusing the target protein (or a ligand binding moiety thereof) to an endogenous protein. It may be that the target protein is endogenous to the host cell, or is substantially identical to an endogenous receptor so that it can take advantage of the latter's native signal transduction pathway. Or sufficient elements of the signal transduction pathway normally associated with the target protein may be engineered into the cell so that the cell signals binding to the target protein.

"One-Hybrid" Systems

In these systems, a chimera receptor, a hybrid of the target protein and an endogenous receptor, is used. The chimeric receptor has the ligand binding characteristics of the target protein and the signal transduction characteristics of the endogenous receptor. Thus, the normal signal transduction pathway of the endogenous receptor is subverted.

Preferably, the endogenous receptor is inactivated, or the conditions of the assay avoid activation of the

endogenous receptor, to improve the signal-to-noise ratio.

See Fowlkes USP 5,789,184 for a yeast system.

Another type of "one-hybrid" system combines a peptide:
DNA-binding domain fusion with an unfused target receptor
5 that possesses an activation domain.

"Two-Hybrid" System

In a preferred embodiment, the cell-based assay is a
two hybrid system. This term implies that the ligand is
10 incorporated into a first hybrid protein, and the receptor
into a second hybrid protein. The first hybrid also
comprises component A of a signal generating system, and the
second hybrid comprises component B of that system.
Components A and B, by themselves, are insufficient to
15 generate a signal. However, if the ligand binds the
receptor, components A and B are brought into sufficiently
close proximity so that they can cooperate to generate a
signal.

Components A and B may naturally occur, or be
20 substantially identical to moieties which naturally occur,
as components of a single naturally occurring biomolecule,
or they may naturally occur, or be substantially identical
to moieties which naturally occur, as separate naturally
occurring biomolecules which interact in nature.

Two-Hybrid System: Transcription Factor Type

In a preferred "two-hybrid" embodiment, one member of a
peptide ligand:receptor binding pair is expressed as a
fusion to a DNA-binding domain (DBD) from a transcription
30 factor (this fusion protein is called the "bait"), and the
other is expressed as a fusion to a transactivation domain
(TAD) (this fusion protein is called the "fish", the "prey",
or the "catch"). The transactivation domain should be
complementary to the DNA-binding domain, i.e., it should
35 interact with the latter so as to activate transcription of
a specially designed reporter gene that carries a binding
site for the DNA-binding domain. Naturally, the two fusion
proteins must likewise be complementary.

This complementarity may be achieved by use of the complementary and separable DNA-binding and transcriptional activator domains of a single transcriptional activator protein, or one may use complementary domains derived from different proteins. The domains may be identical to the native domains, or mutants thereof. The assay members may be fused directly to the DBD or TAD, or fused through an intermediated linker.

The target DNA operator may be the native operator sequence, or a mutant operator. Mutations in the operator may be coordinated with mutations in the DBD and the TAD. An example of a suitable transcription activation system is one comprising the DNA-binding domain from the bacterial repressor LexA and the activation domain from the yeast transcription factor Gal4, with the reporter gene operably linked to the LexA operator.

It is not necessary to employ the intact target receptor; just the ligand-binding moiety is sufficient.

The two fusion proteins may be expressed from the same or different vectors. Likewise, the activatable reporter gene may be expressed from the same vector as either fusion protein (or both proteins), or from a third vector.

Potential DNA-binding domains include Gal4, LexA, and mutant domains substantially identical to the above.

Potential activation domains include E. coli B42, Gal4 activation domain II, and HSV VP16, and mutant domains substantially identical to the above.

Potential operators include the native operators for the desired activation domain, and mutant domains substantially identical to the native operator.

The fusion proteins may comprise nuclear localization signals.

The assay system will include a signal producing system, too. The first element of this system is a reporter gene operably linked to an operator responsive to the DBD and TAD of choice. The expression of this reporter gene will result, directly or indirectly, in a selectable or screenable phenotype (the signal). The signal producing

system may include, besides the reporter gene, additional genetic or biochemical elements which cooperate in the production of the signal. Such an element could be, for example, a selective agent in the cell growth medium. There may be more than one signal producing system, and the system may include more than one reporter gene.

The sensitivity of the system may be adjusted by, e.g., use of competitive inhibitors of any step in the activation or signal production process, increasing or decreasing the number of operators, using a stronger or weaker DBD or TAD, etc.

When the signal is the death or survival of the cell in question, or proliferation or nonproliferation of the cell in question, the assay is said to be a selection. When the signal merely results in a detectable phenotype by which the signaling cell may be differentiated from the same cell in a nonsignaling state (either way being a living cell), the assay is a screen. However, the term "screening assay" may be used in a broader sense to include a selection. When the narrower sense is intended, we will use the term "nonselective screen".

Various screening and selection systems are discussed in Ladner, USP 5,198,346.

Screening and selection may be for or against the peptide: target protein or compound:target protein interaction.

Preferred assay cells are microbial (bacterial, yeast, algal, protozoal), invertebrate, vertebrate (esp. mammalian, particularly human). The best developed two-hybrid assays are yeast and mammalian systems.

Normally, two hybrid assays are used to determine whether a protein X and a protein Y interact, by virtue of their ability to reconstitute the interaction of the DBD and the TAD. However, augmented two-hybrid assays have been used to detect interactions that depend on a third, non-protein ligand.

For more guidance on two-hybrid assays, see Brent and Finley, Jr., Ann. Rev. Genet., 31:663-704 (1997); Fremont-

Racine, et al., Nature Genetics, 277-281 (16 July 1997); Allen, et al., TIBS, 511-16 (Dec. 1995); LeCrenier, et al., BioEssays, 20:1-6 (1998); Xu, et al., Proc. Nat. Acad. sci. (USA), 94:12473-8 (Nov. 1992); Esotak, et al., Mol. Cell. Biol., 15:5820-9 (1995); Yang, et al., Nucleic Acids Res., 23:1152-6 (1995); Bendixen, et al., Nucleic Acids Res., 22:1778-9 (1994); Fuller, et al., BioTechniques, 25:85-92 (July 1998); Cohen, et al., PNAS (USA) 95:14272-7 (1998); Kolonin and Finley, Jr., PNAS (USA) 95:14266-71 (1998). See also Vasavada, et al., PNAS (USA), 88:10686-90 (1991) (contingent replication assay), and Rehrauer, et al., J. Biol. Chem., 271:23865-73 (1996) (LexA repressor cleavage assay).

Two-Hybrid Systems: reporter Enzyme type

In another embodiment, the components A and B reconstitute an enzyme which is not a transcription factor.

As in the last example, the effect of the reconstitution of the enzyme is a phenotypic change which may be a screenable change, a selectable change, or both.

In vivo Diagnostic Uses

Radio-labeled ABM may be administered to the human or animal subject. Administration is typically by injection, e.g., intravenous or arterial or other means of administration in a quantity sufficient to permit subsequent dynamic and/or static imaging using suitable radio-detecting devices. The dosage is the smallest amount capable of providing a diagnostically effective image, and may be determined by means conventional in the art, using known radio-imaging agents as a guide.

Typically, the imaging is carried out on the whole body of the subject, or on that portion of the body or organ relevant to the condition or disease under study. The amount of radio-labeled ABM accumulated at a given point in time in relevant target organs can then be quantified.

A particularly suitable radio-detecting device is a

scintillation camera, such as a gamma camera. A
scintillation camera is a stationary device that can be used
to image distribution of radio-labeled ABM. The detection
device in the camera senses the radioactive decay, the
5 distribution of which can be recorded. Data produced by the
imaging system can be digitized. The digitized information
can be analyzed over time discontinuously or continuously.
The digitized data can be processed to produce images,
called frames, of the pattern of uptake of the radio-labeled
10 ABM in the target organ at a discrete point in time. In
most continuous (dynamic) studies, quantitative data is
obtained by observing changes in distributions of
radioactive decay in target organs over time. In other
words, a time-activity analysis of the data will illustrate
15 uptake through clearance of the radio-labeled binding
protein by the target organs with time.

Various factors should be taken into consideration in
selecting an appropriate radioisotope. The radioisotope
must be selected with a view to obtaining good quality
20 resolution upon imaging, should be safe for diagnostic use
in humans and animals, and should preferably have a short
physical half-life so as to decrease the amount of radiation
received by the body. The radioisotope used should
preferably be pharmacologically inert, and, in the
25 quantities administered, should not have any substantial
physiological effect.

The ABM may be radio-labeled with different isotopes of
iodine, for example ^{123}I , ^{125}I , or ^{131}I (see for example, U.S.
Patent 4,609,725). The extent of radio-labeling must,
30 however be monitored, since it will affect the calculations
made based on the imaging results (i.e. a diiodinated ABM
will result in twice the radiation count of a similar
monoiodinated ABM over the same time frame).

In applications to human subjects, it may be desirable
35 to use radioisotopes other than ^{125}I for labeling in order to
decrease the total dosimetry exposure of the human body and
to optimize the detectability of the labeled molecule
(though this radioisotope can be used if circumstances

require). Ready availability for clinical use is also a factor. Accordingly, for human applications, preferred radio-labels are for example, ^{99m}Tc , ^{67}Ga , ^{68}Ga , ^{90}Y , ^{111}In , ^{113m}In , ^{123}I , ^{186}Re , ^{188}Re or ^{211}At .

5 The radio-labeled ABM may be prepared by various methods. These include radio-halogenation by the chloramine - T method or the lactoperoxidase method and subsequent purification by HPLC (high pressure liquid chromatography), for example as described by J. Gutkowska et al in
10 "Endocrinology and Metabolism Clinics of America: (1987) 16 (1):183. Other known methods of radio-labeling can be used, such as IODOBEADS™.

 There are a number of different methods of delivering the radio-labeled ABM to the end-user. It may be
15 administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. Because proteins are subject to being digested when administered orally, parenteral administration, i.e., intravenous, subcutaneous, intramuscular, would ordinarily
20 be used to optimize absorption of an ABM, such as an antibody, which is a protein.

EXAMPLES

25 Animal Models.

 Obesity and subsequent hyperinsulinemia and hyperglycemia were induced by feeding a group of 3 week old mice (50 C57B1/6 males) a high-fat diet (Bio-Serve, Frenchtown, NJ, #F1850 High Carbohydrate-High Fat). Another
30 group of 3 week old mice (20 C57B1/6 males) were fed the normal control diet (PMI Nutrition International Inc., Brentwood, MO, Prolab RMH3000). The mice were placed onto the respective diets immediately following weaning. Animal weights were determined weekly. Fasting blood-glucose and
35 plasma insulin measurements were determined after 2, 4, 8 and 16 weeks, and 6 months, on the respective diets.

 Normal weight, normal fasting blood glucose and normal fasting plasma insulin levels are defined as the respective

mean values of the animals fed the control diet.

Two of the "most typical" animals were selected for each group (Control, hyperinsulinemic and Diabetic) at each time point (2,4, 8, and 16 weeks, and 6 months, after commencement of diet) for sacrifice. The selected mice were sacrificed and liver tissue obtained and frozen in liquid nitrogen until processed for RNA isolation.

Fasting Blood Glucose Levels.

Blood glucose levels was measured from a drop of blood taken from the tip of the tail of fasted (6 hr) mice using a Lifescan Genuine One Touch glucometer. All measurements occurred between 3:00 pm and 5:00 pm.

Plasma insulin measurements.

Blood was collected from the tail of fasted (6hr) mice into a heparinized capillary tube and stored on ice. All collections occurred between 3:00 pm and 5:00 pm. Plasma was separated from red blood cells by centrifugation for 10 minutes at 8000 x g and then stored at -20°C. Insulin concentrations were determined using the Rat Insulin ELISA kit and rat insulin standards (ALPCO) essentially as instructed by the manufacturer. Values were adjusted by a factor of 1.23 as determined by the manufacturer to correct for the species difference in cross-reactivity with the antibody.

RNA isolation.

Total RNA was isolated from livers using the RNA STAT-60 Total RNA/mRNA Isolation Reagent according to the manufacturer's instructions (Tel-Test, Friendswood, TX).

Sample Quantification and Quality Assessment

Total RNA was quantified and assessed for quality on a Bioanalyzer RNA 6000 Nano chip (Agilent). Each chip contained an interconnected set of gel-filled channels that allowed for molecular sieving of nucleic acids. Pin-

non-overlapping and unrelated. Combinations of the above are also possible.

In addition to the classes stated, the corresponding human gene clusters are also of interest. These may be obtained in a number of ways. First, one may search on Unigene (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>) for the identified human protein. Review the "hits" (each of which is a Unigene record) for those prefixed by "Hs." Secondly, one may access the Unigene record for the mouse gene cluster (which is given in Master Table 1), and then click on "Homologene". This will bring up a new page which includes the section "Possible Homologous Genes". One of the entries should be a Homo sapiens gene (considered by Unigene to be the most related human gene); click on its Unigene record link.

Additional information of interest may be accessed by searching with the mouse gene accession # in the Mouse Gene Informatics database, at <http://www.informatics.jax.org/>.

Master Table 1: Subtable 1A Favorable Genes/Proteins

Mouse Gene Protein	Umigene	Behavior	Human Protein	Human Protein Name	Score	E-Value
NM_007630	Mm.22592	F:(HI-D)	NP_004692.1	cyclin B2	694	0
NP_031656.1		-5.28				
			NP_114172.1	cyclin B1; G2/mitotic-specific cyclin B1	382	1.00e-106
			XP_172630.1	similar to cyclin B2	239	6.00e-63
NM_007913	Mm.18195	F:(HI-D)	NP_001955.1	early growth response 1; G0S30	783	0
NP_031939.1	9	-2.66				
			XP_005040.2	similar to Early growth response protein 3 (EGR-3) (Zinc finger protein pilot)	275	3.00e-73
			NP_004421.1	early growth response 3	274	6.00e-73
AF127033	Mm.3760	F:(HI-D)	NP_004095.3	fatty acid synthase		
AAG02285.1		-2.1			3961	0
			G01880	fatty-acid synthase (EC 2.3.1.85) (version 2)	3945	0
			P49327	Fatty acid synthase [Includes: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]	3778	0
			B57788	fatty-acid synthase (EC 2.3.1.85) (HepG2 cell variant)	3740	0
			AAH07267.1	Unknown (protein for IMAGE:3138929)	1533	0
			AAB35516.1	fatty acid synthase; FAS [Homo sapiens]	728	0
			AAH07305.1	Unknown (protein for MGC:15706)	685	0
			AAH14634.1	Unknown (protein for IMAGE:3535581)	553	1.00e-156
NM_011169	Mm.2752	F:(HI-D)	NP_000940.1	prolactin receptor		
NP_035299.1		-2.08			789	0
			AAK32703.1	prolactin receptor isoform delta S1 precursor	605	1.00e-173
			AAL23915.1	prolactin receptor short isoform 1a	512	1.00e-145
			AAD49855.1	intermediate prolactin receptor isoform	509	1.00e-144
			AAL23914.1	prolactin receptor short isoform 1b	448	1.00e-125

NM_013490	Mm.5262	F:(HI-D)	AAH36471.1	Similar to choline kinase	679	0
NP_038518.1		-2.04				
			NP_001268.1	choline kinase	665	0
			NP_005189.2	choline/ethanolamine kinase isoform a	433	1.00e-121
NM_013888	Mm.32550	F:(HI-D)	NP_068572.1	J domain containing protein 1		
NP_038916.1		-2.04			310	3.00e-84
NM_019499	Mm.43444	F:(HI-D)	NP_002349.1	MAD2-like 1; MAD2 (mitotic arrest deficient, yeast, homolog)-like 1; mitotic arrest		
NP_062372.1		-2.04		deficient, yeast, homolog-like 1	382	1.00e-106
			21465465	Chain A, Crystal Structure Of Mad1-Mad2 Reveals A Conserved Mad2 Binding Motif In Mad1 And Cdc20	380	1.00e-102
			18655665	Chain A, The Mad2 Spindle Checkpoint Protein Undergoes Similar Major Conformational Changes Upon Binding To Either Mad1 Or Cdc20	368	1.00e-102
			7245371	Chain A, Solution Structure Of The Spindle Assembly Checkpoint Protein Human Mad2	348	5.00e-96
NM_011850	Mm.34209	F:(HI-D)	NP_068804.1	short heterodimer partner; orphan nuclear receptor SHP; small heterodimer		
NP_035980.1		-2.03		partner; nuclear receptor subfamily 0, group B, member 2	404	1.00e-112
			AAC41998.1	nuclear hormone receptor	402	1.00e-112
AF213393	Mm.38377	F:(HI-D)	NP_009099.1	ATP-binding cassette, sub-family A member 8		
AAF31432.1		-2.02			280	2.00e-75
			NP_525022.1	ATP-binding cassette, sub-family A (ABC1), member 9	267	2.00e-71
			AAN32751.1	ATP-binding cassette sub-family A member 9	267	2.00e-71
			NP_525021.1	ATP-binding cassette, sub-family A (ABC1), member 10	244	8.00e-65
			AAM77557.1	ABC transporter ABCA6	227	2.00e-59
			NP_525023.1	ATP-binding cassette, sub-family A (ABC1), member 6	227	2.00e-59
			BAC04994.1	unnamed protein product	227	2.00e-59
			CAB93535.3	ATP-binding cassette protein	199	3.00e-51
			NP_061142.1	ATP-binding cassette protein of the (ABCA subfamily)	199	3.00e-51
			BAB71700.1	unnamed protein product	199	3.00e-51
			BAB67781.1	KIAA1888 protein	199	3.00e-51

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			BAB71208.1	unnamed protein product	199	7.00e-51
NM_013646	Mm.8858	F:(HI-D)	NP_599023.1	RAR-related orphan receptor A, isoform a; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	954	0
NP_038674.1			NP_002934.1	RAR-related orphan receptor A, isoform c; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0
			NP_599022.1	RAR-related orphan receptor A, isoform b; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0
			NP_599024.1	RAR-related orphan receptor A, isoform d; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha	896	0
			A56856	retinoid-related orphan receptor RZR-alpha - human	893	0
			NP_008845.2	RAR-related orphan receptor B; RAR-related orphan receptor beta; retinoic acid-binding receptor beta; nuclear receptor RZR-beta	561	1.00e-160
			CAD13276.1	bA133M9.1 (RAR-related orphan receptor B)	561	1.00e-159
			Q92753	NUCLEAR RECEPTOR ROR-BETA (NUCLEAR RECEPTOR RZR-BETA)	559	1.00e-159
NM_009425	Mm.1062	F:(HI-D)	NP_003801.1	tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related apoptosis inducing ligand TRAIL	345	9.00e-95
NP_033451.1		-10.21	6980394	Chain A, Crystal Structure Of Apo2/TRAIL	266	4.00e-71
			6435529	Chain B, Crystal Structure Of Trail-Dr5 Complex	248	2.00e-65
			10835510	Chain D, Crystal Structure Of Trail-Sdr5	248	2.00e-65
AK018485		F:(C-HI)-				
2204249A	Mm.23336	2.45	NP_699169	hypothetical protein FLJ90165	211	5.00e-90

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NM_008182	Mm.19742	F:(C-HI)	NP_665683.1	glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-aryltransferase A1; GST-epsilon; glutathione S-transferase 2	328	8.00e-90
NP_032208.1	2	-9.17, F:(C-D) -5.68	IS2381	glutathione transferase (EC 2.5.1.18) - human	327	1.00e-89
			DAA00071.1	TPA: glutathione transferase A5	327	1.00e-89
			442977	Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)	326	3.00e-89
			1127144	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k)	325	6.00e-89
			XP_167100.2	similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha)	325	6.00e-89
			Q16772	Glutathione S-transferase A3-3 (GST class-alpha)	324	1.00e-88
			NP_000838.2	glutathione S-transferase A3	322	3.00e-88
			A49365	glutathione transferase (EC 2.5.1.18) alpha-3 [similarity] - human	322	4.00e-88
			AAA74634.1	glutathione S-transferase A3	322	4.00e-88
			S20331	glutathione transferase (EC 2.5.1.18) - human	318	5.00e-87
			S27110	glutathione transferase (EC 2.5.1.18) A2 - human	317	1.00e-86
			S24330	thione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human	316	3.00e-66
			NP_000837.2	thione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-aryltransferase A2; GST-gamma; HA subunit 2	315	4.00e-86
			CAB92770.1	dJ152L7.3 (glutathione S-transferase A2)	315	4.00e-86
			S77958	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2 (+)) - human	309	3.00e-84
			A56801	glutathione transferase (EC 2.5.1.18) alpha y - human	309	4.00e-84
NM_028089	Mm.14258	F:(C-HI)	NP_000763.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18;		
NP_082365.1	1	-4.31, F:(C-D) -5.26		cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	766	0
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	764	0

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				AAB23864.2	cytochrome P-450		736	0
				NP_000762.2	hrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		736	0
				BAA00123.1	cytochrome P-450		736	0
				P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)		729	0
				AA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase		729	0
				226295	cytochrome P450		728	0
				NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		726	0
				F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human		722	0
				P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)		709	0
				AAH20596.1	Unknown (protein for MGC:22146)		707	0
				AA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase		706	0
				NP_000761.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1		706	0
				S66382	cytochrome P450 2C8 - human		704	0
				AAB35292.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]		704	0
				AA52161.1	cytochrome P-450 S-mephenytoin 4-hydroxylase		696	0
				I52418	cytochrome P450 - human		662	0
				G38462	chrome P450 2C17 - human (fragment)		593	1.00e-169

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NM_007818 NP_031844.1	Mm.21193	F:(C-HI) -4.29, F:(C-D) -8.15	NP_000768.1	cytochrome P450, subfamily IIIA, polypeptide 5; nifedipine oxidase; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase	726	0
			NP_059488.2	cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3	724	0
			P08684	Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP3A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)	723	0
			NP_000767.1	cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3	723	0
			AAA35744.1	cytochrome P-450 nifedipine oxidase	722	0
			AAF13598.1	cytochrome P450-3A4	715	0
			AAA35747.1	cytochrome P450 nifedipine oxidase	711	0
			NP_000756.1	cytochrome P450, subfamily IIIA, polypeptide 7; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	698	0
			AAG48618.1	cytochrome P450 variant 3A7	693	0
			NP_476436.1	cytochrome P450 polypeptide 43 isoform 2; cytochrome P450 polypeptide 43	644	0
			NP_073731.1	cytochrome P450 polypeptide 43 isoform 1; cytochrome P450 polypeptide 43	639	0
			NP_476437.1	cytochrome P450 polypeptide 43 isoform 3; cytochrome P450 polypeptide 43	525	1.00e-149
			AAG33012.1	cytochrome P450 subfamily IIIA polypeptide 43	284	2.00e-76
			AAF99272.1	thromboxane synthase	278	1.00e-74
			AAF99279.1	thromboxane synthase	278	2.00e-74
			AAF99274.1	thromboxane synthase	277	3.00e-74
			AAF99278.1	thromboxane synthase	277	3.00e-74
			AAF99276.1	thromboxane synthase	277	4.00e-74
			NP_001052.1	thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V), isoform TXS-i; TXA synthase	277	4.00e-74
			AAF99275.1	thromboxane synthase	277	4.00e-74
			P24557	Thromboxane-A synthase (TXA synthase) (TXS)	276	5.00e-74

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			thromboxane-A synthase (EC 5.3.99.5) - human	276	5.00e-74
			thromboxane synthase	276	8.00e-74
			thromboxane synthase	275	1.00e-73
			thromboxane synthase	275	1.00e-73
			thromboxane synthase	248	2.00e-65
			Unknown (protein for MGC:20885)	204	4.00e-52
			thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V), isoform		
			thromboxane synthase		
			TXS-II; TXA synthase	498	1.00e-140
			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	276	6.00e-74
			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 9 (ovalbumin type)	275	1.00e-73
			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 10 (ovalbumin type, bomapin)	275	2.00e-73
			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 8 (ovalbumin type)	272	1.00e-72
			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	269	9.00e-72
			serine (or cysteine) proteinase inhibitor - human	267	3.00e-71
			inhibitor 6 (placental thrombin inhibitor)	266	8.00e-71
			placental thrombin inhibitor - human		
			leupin precursor - human		
			leupin precursor cell carcinoma antigen 2 (SCCA-2) (Leupin)		
			similar to Squamous cell carcinoma Inhibitor-2.[loop (66-98) Deletionmutant] Complexed	265	2.00e-70
			Human Plasminogen Activator Inhibitor-2.[loop (66-98) Deletionmutant] Complexed	264	3.00e-70
			With Peptide Mimicking The Reactive Center Loop		
			squamous cell carcinoma antigen 1		
			squamous cell carcinoma antigen 1		

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NM_008341	Mm.21300	F:(C-HI)	AAH35263.1	Similar to insulin-like growth factor binding protein 1		
NP_032367.1		-3.37, F:(C-D) -3.47, F:(HI-D) -2.63			384	1.00e-106
			CAA68770.1	IGF-binding preprotein (AA -25 to 234)	384	1.00e-106
			NP_000587.1	insulin-like growth factor binding protein 1	382	1.00e-106
			AAA52540.1	insulin-like growth factor binding protein 1	338	9.00e-93
			CAA33110.1	small IGF-binding-protein	196	5.00e-50
U38940	Mm.2942	F:(C-HI)	NP_001664.2	asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell		
AAA85125.1		-3.11, F:(C-D) -2.11		cycle control protein	1035	0
			P08243	Asparagine synthetase [glutamine-hydrolyzing] (Glutamine-dependent asparagine synthetase) (TS11 cell cycle control protein)	1033	0
			AJHUNI	aspartate-ammonia ligase (EC 6.3.1.1) - human	1030	0
			XP_095404.4	similar to asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein	562	1.00e-160
J03953	Mm.37199	F:(C-HI)	4388890	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a	352	4.00e-97
AAA37748.1		-3.03	XP_002155.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4)	352	4.00e-97
			AAA59203.1	(GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)	350	2.00e-96
			4557966	glutathione transferase M1	348	1.00e-95
				Chain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form		

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NP_000839.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	348	1.00e-95
494185	Chain , Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	344	1.00e-94
6980588	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	342	7.00e-94
NP_000841.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	342	7.00e-94
AAA57346.1	glutathione transferase M4	340	2.00e-93
S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2)	338	8.00e-93
P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	337	1.00e-92
NP_000842.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	336	3.00e-92
CAA48636.1	glutathione S-transferase	302	6.00e-82
AAH17836.1	Similar to glutathione S-transferase M2 (muscle)	299	5.00e-81
XP_042722.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	297	2.00e-80
AAH08790.1	Unknown (protein for MGC:3704)	297	2.00e-80
5822511	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	297	2.00e-80
NP_671489.1	hione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	296	3.00e-80

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				A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3	294	2.00e-79
				XP_167023.1	similar to glutathione transferase M2	277	2.00e-74
				NP_666533.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	270	2.00e-72
NM_013459	Mm.4407	F:(C-HI)		P00746	Complement factor D precursor (C3 convertase activator) (Properdin factor D)	370	1.00e-102
NP_038487.1		-2.94		CAC48304.1	(Adipsin)	358	4.00e-99
				67580	adipsin/complement factor D precursor	352	5.00e-97
				6730437	complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)	340	1.00e-93
				1633237	Chain A, Proenzyme Of Human Complement Factor D, Recombinant Profactor D	330	1.00e-90
				5542120	Chain , Mutant Of Factor D With Enhanced Catalytic Activity	329	3.00e-90
				XP_084037.1	Chain , Human Complement Factor D In Complex With Isatoic Anhydride Inhibitor		
					similar to Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)	328	8.00e-90
				NP_001919.1	adipsin/complement factor D precursor	324	1.00e-88
NM_016810	Mm.20931	F:(C-HI)		NP_004862.1	golgi SNAP receptor complex member 1; Golgi SNARE 28 kDa	477	1.00e-134
NP_058090.1		-2.86					
				AAC39889.1	GOS28/P28 protein	452	1.00e-127
				AAH12620.1	Similar to golgi SNAP receptor complex member 1	218	1.00e-56
AK006128	Mm.23942	F:(C-HI)		AAD01430.1	MRP3	365	1.00e-101
BAB24422.1		-2.71		AAD38185.1	MRP3s1 protein	365	1.00e-101
				NP_003777.2	ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter	365	1.00e-101
				CAA76658.2	multidrug resistance protein 3 (ABCC3)	365	1.00e-101
				BAA28146.1	multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2)	365	1.00e-101
				JB0336	canalicular multispecific organic anion transporter	364	1.00e-100
				AAB71756.1	multidrug resistance-associated protein homolog	350	2.00e-96
				CAC69553.1	multidrug resistance associated protein	331	1.00e-90
				AAH01636.1	Unknown (protein for IMAGE:3355848)	313	3.00e-85

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			NP_063954.1	ATP-binding cassette, sub-family C, member 1, isoform 4; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			AAB83979.1	multidrug resistance protein	313	3.00e-85
			NP_063953.1	ATP-binding cassette, sub-family C, member 1, isoform 3; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			NP_004987.1	ATP-binding cassette, sub-family C, member 1, isoform 1; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			DVHUAR	multidrug resistance protein (cell line H69AR)	313	3.00e-85
			NP_063915.1	ATP-binding cassette, sub-family C, member 1, isoform 2; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			NP_063957.1	ATP-binding cassette, sub-family C, member 1, isoform 7; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			AAC15784.1	Multiple drug resistance gene MRP1 (5' partial)	313	3.00e-85
			AAB83982.1	multidrug resistance protein	313	3.00e-85
			AAB83980.1	multidrug resistance protein	313	3.00e-85
			NP_063956.1	ATP-binding cassette, sub-family C, member 1, isoform 6; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein	313	3.00e-85
			AAB83981.1	multidrug resistance protein	313	3.00e-85
			AAB09422.1	canalicular multispecific organic anion transporter	279	5.00e-75
			NP_000383.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 2; canalicular multispecific organic anion transporter	277	2.00e-74
			S71841	multidrug resistance protein, canalicular	276	3.00e-74
			CAB45309.1	multidrug resistance protein 2 (MRP2)	276	3.00e-74
NM_008742	Mm.20070	F:(C-HI)	NP_002518.1	neurotrophin 3 precursor	449	1.00e-141
NP_032768.1	3	-2.68				
			5542321	Chain A, Human Neurotrophin-3	255	5.00e-68
			1421251	Chain B, Neurotrophin Mol_id: 1; Molecule: Brain Derived Neurotrophic Factor; Chain: A; Synonym: Bdnf; Engineered: Yes; Mol_id: 2; Molecule: Neurotrophin 3; Chain: B; Synonym: NT3; Engineered: Yes; Other_details: Heterodimer	249	4.00e-66

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NM_008361	Mm.22150	F:(C-HI) -2.65, F:(C-D) -2.03	NP_000567.1	interleukin 1, beta		
NP_032387.1					352	3.00e-97
			P01584	Interleukin-1 beta precursor (IL-1 beta) (Catabolin)	350	1.00e-96
			AAA59136.1	interleukin 1	345	6.00e-95
			AAC03536.1	interleukin 1 beta	240	2.00e-63
			1827779	Chain , Interleukin-1 Beta From Joint X-Ray And Nmr Refinement	239	2.00e-63
			230947	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 8 Replaced By Ala (C8A)	239	3.00e-63
			494152	Chain , Interleukin-1 Beta (Human) Mutant With Thr 9 Replaced By Gly (T9g)	239	3.00e-63
			230410	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 71 Replaced By Ala) (C71A)	236	3.00e-62
			230798	Chain , Interleukin-1Beta (IL-1Beta) (Mutant With Cys 71 Replaced By Ser) (C71S)	236	4.00e-62
AF294617	Mm.19669	F:(C-HI) -2.63	NP_004557.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase		
AAG02118.1					1030	0
			AAB99795.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	1028	0
			JC4626	6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate		
				2-phosphatase (EC 3.1.3.46)	1028	0
			AAC62000.1	inducible 6-phosphofructo-2-kinase/fructose 2,6-bisphosphatase	1005	0
			CAA06605.1	6-phosphofructo-2-kinase	699	0
			O60825	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 (6PF-2-K/Fru-2,6-P2ASE heart-type isozyme) (PFK-2/FBPase-2) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase]	697	0
			NP_006203.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2;		
				Fructose-2,6-bisphosphatase, cardiac isozyme	688	0
			BAB19681.1	6-phosphofructo-2-kinase heart isoform	680	0
			NP_004558.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	670	0
			JC5871	6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate		
				2-phosphatase (EC 3.1.3.46)	669	0
			NP_002616.1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1;		
				Fructose-2,6-bisphosphatase	668	0

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				PI6118	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase]	668	0
				CAB06077.1	6-phosphofructo-2-kinase	589	1.00e-167
NM_009998	Mm.14177	F:(C-HI)		NP_000758.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6		
NP_034128.1		-2.61, F:(C-D)					
		-2.33				701	0
				AAF13602.1	cytochrome P450-2B6	692	0
				AAA52143.1	cytochrome P450-IIB	511	1.00e-144
NM_008988	Mm.10689	F:(C-HI)		XP_116965.2	similar to punc		
NP_033014.1		-2.6				695	0
				NP_066013.1	DDM36	390	1.00e-108
				AAD13399.1	putative neuronal cell adhesion molecule	384	1.00e-106
				AAA35751.1	colorectal tumor suppressor (put.); putative	254	7.00e-67
				NP_005206.1	deleted in colorectal carcinoma	254	7.00e-67
NM_010166	Mm.1430	F:(C-HI)		Q99504	Eyes absent homolog 3		
NP_034296.1		-2.57				778	0
				CAA71311.1	EYA3	763	0
				NP_001981.1	eyes absent homolog 3 (Drosophila);	644	0
				AAH14193.1	Unknown (protein for IMAGE:4110403)	438	1.00e-122
				NP_004091.1	eyes absent homolog 4 (Drosophila);	436	1.00e-122
				NP_000494.2	eyes absent 1 isoform b; Eyes absent, Drosophila, homolog of, 1; Melnick-Fraser syndrome		
				CAA71309.1	EYA1A	431	1.00e-120
				AAH08803.1	Similar to eyes absent (Drosophila) homolog 2	431	1.00e-120
				AAH00289.1	Similar to eyes absent (Drosophila) homolog 2	399	1.00e-110
				O00167	Eyes absent homolog 2	394	1.00e-109
				AAC09362.1	eyes absent homolog	394	1.00e-109
				NP_005235.2	eyes absent homolog 2	394	1.00e-109
				AAI73437.1	EYA1D	392	1.00e-108
						380	1.00e-104

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AK002480	Mm.28301	F:(C-HI)	AAB42065.1	EYA2 homolog	318	3.00e-86
NP_666065.1		-2.55, F:(C-D) -2.57	NP_001893.2	cystathionase isoform 1; cystathionine gamma-lyase; homoserine deaminase; homoserine dehydratase; cysteine desulphydrase		
			P32929	Cystathionine gamma-lyase	574	1.00e-163
			CAC12901.1	bA42O15.1.2 (cystathionase (cystathionine gamma-lyase))	574	1.00e-163
			JC1362	cystathionine gamma-lyase (EC 4.4.1.1)	480	1.00e-135
AK018226	Mm.92685	F:(C-HI)	NP_109591.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived	480	1.00e-135
XP_110043.1		-2.53, F:(C-D) -2.4				
			NP_004146.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)	345	1.00e-138
			NP_002631.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	200	5.00e-79
			NP_005015.1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)	207	2.00e-76
			NP_004559.2	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)	179	4.00e-75
			15988197	Chain A, Human Plasminogen Activator Inhibitor-2.[loop (66-98) Deletionmutant] Complexed With Peptide Mimicking The Reactive Center Loop	192	4.00e-75
			539661	placental thrombin inhibitor - human		
NM_010361	Mm.24118	F:(C-HI)	NP_000845.1	glutathione S-transferase theta 2	199	5.00e-75
NP_034491.1		-2.46, F:(C-D) -2.25			190	3.00e-74
			AAG02373.1	glutathione S-transferase theta 2		
			AAC13317.1	glutathione S-transferase theta 2	375	1.00e-104
					375	1.00e-104
					364	1.00e-101

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			XP_056016.1	similar to Glutathione S-transferase theta 1 (GST class-theta) (Glutathione transferase T1-1)	239	3.00e-63
			NP_000844.1	glutathione S-transferase theta 1	239	4.00e-63
			AAH07065.1	glutathione S-transferase theta 1	236	2.00e-62
AK018485	Mm.23336	F:(C-HI) -2.46	XP_064383.2	similar to data source:SPTR, source key:Q60928, evidence:ISS~putative~similar to GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYL TRANSFERASE) (GGT)	261	1.00e-105
			NP_699169.1	hypothetical protein FLJ90165	211	5.00e-90
NM_010924	Mm.8362	F:(C-HI) -2.45;	NP_006160.1	nicotinamide N-methyltransferase		
NP_035054.1		F:(C-D) -2.19			458	1.00e-129
			AAD04723.1	thioether S-methyltransferase-like; similar to P40936 (PID:g731019)	268	1.00e-71
			O95050	Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)	266	3.00e-71
			NP_006765.3	indolethylamine N-methyltransferase; thioester S-methyltransferase-like	265	6.00e-71
			AAH33813.1	Unknown (protein for IMAGE:5209218)	263	2.00e-70
NM_021307	Mm.82678	F:(C-HI) -2.44	AAG23968.1	ZNF228 protein	1078	0
NP_067282.1			XP_009363.3	similar to ZNF228 protein	1078	0
			NP_037512.1	zinc finger protein 228	1073	0
			NP_057528.1	zinc finger protein 226; Kruppel-associated box protein	621	1.00e-177
			Q9NYT6	Zinc finger protein 226	621	1.00e-177
			AAF88103.1	zinc finger protein 226	619	1.00e-176
			NP_004225.2	zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93;		
				zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)	579	1.00e-165
			AAF88107.1	Hypothetical zinc finger-like protein	579	1.00e-164

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			XP_091906.2	similar to Zinc finger protein 229	550	1.00e-156
			AAF76875.1	zinc finger protein	539	1.00e-152
			NP_003416.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain	533	1.00e-151
			AAF63030.1	Zinc finger protein ZNF45	530	1.00e-150
NM_008295	Mm.17910	F:(C-HI)	NP_000853.1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1;		
NP_032321.1		-2.43, F:(C-D) -5.64, F:(HI-D) -2.32		Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid		
			AAA51831.1	3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4-isomerase	528	1.00e-149
			NP_000189.1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2;	526	1.00e-149
				Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid	513	1.00e-145
			AAA36001.1	3-beta-hydroxysteroid dehydrogenase gene	481	1.00e-136
			CAC19801.1	dJ871G17.4 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	360	3.00e-99
			AAM08704.1	3-beta-hydroxysteroid dehydrogenase	353	5.00e-97
			XP_060821.1	similar to dJ871G17.4 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	335	1.00e-91
			XP_060827.5	similar to 3-beta-hydroxysteroid dehydrogenase	258	2.00e-68
			XP_089334.1	similar to 3 BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5-->4-ISOMERASE (3BETA-HSD)		
				3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	238	1.00e-62
			AA37824.1	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	225	2.00e-58
			NP_079469.2	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase	223	8.00e-58
			XP_060822.5	similar to dJ871G17.6 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	213	6.00e-55
			CAC19803.1	dJ871G17.6 (novel 3-beta hydroxysteroid dehydrogenase/isomerase family member)	202	8.00e-52
			AAD14414.1	3 beta-hydroxysteroid dehydrogenase homolog pseudogene	199	7.00e-51

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NM_010001	Mm.38963	F:(C-HI) -2.43, F:(C-D) -2.56	NP_000763.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	669	0
			P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	667	0
			NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	653	0
			BAA00123.1	cytochrome P-450	650	0
			NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	650	0
			AAB23864.2	cytochrome P-450	650	0
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	648	0
			I506290A	cytochrome P450	646	0
			P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	645	0
			AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	645	0
			I52418	cytochrome P450 - human	629	1.00e-180
			P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	624	1.00e-178
AK012213 BAB28101.1	Mm.24457	F:(C-HI) -2.39, F:(C-D) -2.05	A40872	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 5 precursor, mitochondrial		
			CAD13246.1	bA113O24.2 (aldehyde dehydrogenase 1 family, member B1 (ALDH5 ALDHX))	948	0
			NP_000683.2	aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5	947	0
			P30837	Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)	944	0

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			XP_007012.1	similar to Aldehyde dehydrogenase, mitochondrial precursor (ALDH class 2) (ALDH1) (ALDH-E2)	756	0
			6137677	Chain A, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	756	0
			AAA51693.1	aldehyde dehydrogenase	755	0
			NP_000681.1	aldehyde dehydrogenase 2 family (mitochondrial); aldehyde dehydrogenase 2, mitochondrial	741	0
			CAA68290.1	precursor polypeptide (AA -36 to 479)	738	0
			O94788	Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	684	0
			NP_003879.1	aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2	684	0
			AAC51652.1	aldehyde dehydrogenase 1	655	0
			NP_000680.2	aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1	655	0
			NP_000684.1	aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6	650	0
			AAB59500.1	aldehyde dehydrogenase 2 (EC 1.2.1.3)	604	1.00e-172
			AAH30589.1	Similar to aldehyde dehydrogenase 1 family, member A2	599	1.00e-171
			BAA34786.1	RALDH2-T	598	1.00e-170
			I39431	aldehyde dehydrogenase 1 - human (fragment).	467	1.00e-131
			NP_036322.2	formyltetrahydrofolate dehydrogenase isoform a	438	1.00e-122
			XP_090294.1	similar to 10-formyltetrahydrofolate dehydrogenase	434	1.00e-121
			O75891	10-formyltetrahydrofolate dehydrogenase (10-FTHFDH)	433	1.00e-121
			AAH08250.1	Similar to RIKEN cDNA 0610025L15 gene		
NM_023154	Mm.29553	F:(C-HI)				
NP_075643.1		-2.39, F:(C-D)				
		-2.48			456	1.00e-128
			AAG09063.1	protein expressed in thyroid	437	1.00e-123
			NP_055112.1	protein expressed in thyroid	434	1.00e-122

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NM_010401	Mm.13000	F:(C-HI)	BAB61863.1	histidase		
NP_034531.1		-2.39, F:(C-D)			1216	0
		-2.21			1215	0
NM_023455	Mm.15478	F:(C-HI)	NP_002099.1	histidine ammonia-lyase; Histidine ammonia-lyase (histidase)		
NP_075944.1	2	-2.39, F:(C-D)	NP_057431.1	putative N-acetyltransferase Camello 2		
		-2.04			223	4.00e-58
			NP_003951.2	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene	216	3.00e-56
			BAA71643.1	GLA	216	4.00e-56
			AAH12626.1	kidney- and liver-specific gene	214	1.00e-55
			T44342	hypothetical protein TSC501	214	1.00e-55
NM_018779	Mm.10372	F:(C-HI)	CAA06304.1	phosphodiesterase 3A		
NP_061249.1	8	-2.35, F:(C-D)				
		-2.43			1379	0
			Q14432	cGMP-inhibited 3',5'-cyclic phosphodiesterase A (Cyclic GMP inhibited phosphodiesterase A) (CGI-PDE A)	1379	0
			NP_000912.2	phosphodiesterase 3A, cGMP-inhibited	1379	0
			A44093	cGMP-inhibited cAMP phosphodiesterase (EC 3.1.4.-), myocardial form - human	1378	0
			CAA64774.1	cyclic nucleotide phosphodiesterase	677	0
			NP_000913.1	phosphodiesterase 3B, cGMP-inhibited	677	0
AK009563	Mm.28697	F:(C-HI)	XP_045585.1	similar to RIKEN cDNA 2310032D16		
BAB26361.1		-2.33			929	0
			BAA92672.1	KIAA1434 protein	929	0
			BAA91994.1	unnamed protein product	444	1.00e-124

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NM_009466	Mm.10709	F:(C-HI)	NP_003350.1	UDP-glucose dehydrogenase		
NP_033492.1		-2.32, F:(C-D)			971	0
		-2.00	JE0353	uridine diphosphoglucose dehydrogenase (EC 1.-.-)	958	0
			AAC05135.1	UDP glucose 6-dehydrogenase	337	4.00e-92
			CAB98179.1	uridine diphospho-glucose dehydrogenase	320	7.00e-87
			CAB98178.1	uridine diphospho-glucose dehydrogenase	288	2.00e-77
NM_013584	Mm.3174	F:(C-HI)	NP_002301.1	leukemia inhibitory factor receptor precursor		
NP_038612.1		-2.31, F:(C-D)				
		-2.46	AAB23884.1	leukaemia inhibitory factor receptor, LIF receptor [human, placenta, Peptide, 1078 aa]	1663	0
					1640	0
			NP_003990.1	oncostatin M receptor	345	2.00e-94
			AAB61897.1	leukemia inhibitory factor receptor	282	2.00e-75
NM_008061	Mm.18064	F:(C-HI)	NP_000142.1	glucose-6-phosphatase, catalytic		
NP_032087.1		-2.28, F:(C-D)				
		-2.14			588	1.00e-168
			AAH20700.1	Unknown (protein for MGC:22459)	416	1.00e-115
			NP_066999.1	islet-specific glucose-6-phosphatase catalytic subunit-related p	318	2.00e-86
NM_025631	Mm.46448	F:(C-HI)	NP_079503.1	hypothetical protein dJ726C3.2 [
NP_079907.1		-2.25, F:(C-D)				
		-2.16	AAH34415.1	hypothetical protein dJ726C3.2	558	1.00e-159
					555	1.00e-158

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NM_025631		F:(C-HI) -2.25, F:(C-D)					
NP_079907.1	Mm.46448	-2.16	NP_079503.1	hypothetical protein dJ726C3.2 [558	1.00e-159
			AAH34415.1	hypothetical protein dJ726C3.2		555	1.00e-158
NM_025404	Mm.5376	F:(C-HI) -2.24, F:(C-D)	AAH00043.1	ADP-ribosylation factor 4-like			
NP_079680.1		-2.03				359	6.00e-99
			NP_001652.1	ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6		357	2.00e-98
			AAA93229.1	ADP-ribosylation factor		348	1.00e-95
			XP_045890.2	similar to ADP-ribosylation factor 4L		245	4.00e-70
			NP_005729.1	ADP-ribosylation factor-like 4		233	4.00e-61
			NP_005728.2	ADP-ribosylation factor-like 7		222	8.00e-58
			XP_166703.1	similar to ADP-ribosylation-like 4		213	5.00e-55
			BAA75473.1	ADP ribosylation factor-like protein		209	1.00e-53
NM_008615	Mm.14815	F:(C-HI) -2.22	JC4160	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP) (EC 1.1.1.40)		1013	0
NP_032641.1	5		AAB01380.1	NADP-dependent malic enzyme		1013	0
			NP_002386.1	cytosolic malic enzyme 1; malic enzyme, cytoplasmic; malic enzyme 1, soluble;			
				NADP-dependent malic enzyme; malate dehydrogenase; pyruvic-malic carboxylase		977	0
			AAC50613.1	cytosolic NADP(+)-dependent malic enzyme		974	0
			NP_006671.1	malic enzyme 3, NADP(+)-dependent, mitochondrial; malic enzyme,			
				NADP+-dependent, mitochondrial; pyruvic-malic carboxylase; malate			
				dehydrogenase; NADP-ME		799	0
			AAH22472.1	malic enzyme 3, NADP(+)-dependent, mitochondrial		796	0
			NP_002387.1	malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochondrial;			
				malic enzyme 2, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase		624	1.00e-178

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NM_026104	Mm.14883	F:(C-HI)	XP_085281.2	similar to RIKEN cDNA 170095F04	305	1.00e-82
NP_080380.1	7	-2.22			229	4.00e-60
			BAC04065.1	unnamed protein product		
NM_008792	Mm.1247	F:(C-HI)	NP_002585.2	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone		
NP_032818.1		-2.19		convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like	1247	0
				endoprotease 2; proprotein convertase PC5	1244	0
			AAA60032.1	endoprotease	892	0
			CAB89428.1	dJ531H16.1 (proprotein convertase subtilisin/kexin type 2 (NEC2))		
			NP_000430.3	proprotein convertase subtilisin/kexin type 1 preproprotein; prohormone convertase		
				3; prohormone convertase 1; neuroendocrine convertase 1; proprotein convertase	509	e-144
				1		
NM_013743	Mm.10283	F:(C-HI)	NP_002603.1	pyruvate dehydrogenase kinase, isoenzyme 4	764	0
NP_038771.1		-2.19			562	1.00e-159
			NP_002601.1	pyruvate dehydrogenase kinase, isoenzyme 1	556	1.00e-158
			NP_002602.2	pyruvate dehydrogenase kinase, isoenzyme 2	554	1.00e-157
			I70159	pyruvate dehydrogenase (lipoamide)] kinase (EC 2.7.1.99) 2	527	1.00e-149
			NP_005382.1	pyruvate dehydrogenase kinase, isoenzyme 3		
NM_010357	Mm.2662	F:(C-HI)	Q16772	Glutathione S-transferase A3-3 (GST class-alpha)		
NP_034487.1		-2.17, F:(C-D)			264	1.00e-70
		-2.93			263	3.00e-70
			NP_000838.2	glutathione S-transferase A3	261	1.00e-69
			A49365	glutathione transferase (EC 2.5.1.18) alpha-3 [similarity]		
			NP_665683.1	glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase		
				A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1;	261	1.00e-69
				glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2	261	1.00e-69
			AAA74634.1	glutathione S-transferase A3	259	3.00e-69
			S27110	glutathione transferase (EC 2.5.1.18) A2	259	4.00e-69
			S24330	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human	259	5.00e-69
			CAB92770.1	dJ152L7.3 (glutathione S-transferase A2)	259	5.00e-69

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			442977	Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)	259	5.00e-69
			NP_000837.2	glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-aralkyltransferase A2; GST-gamma; HA subunit 2	258	6.00e-69
			1127144	Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k)	258	2.00e-68
			S20331	glutathione transferase (EC 2.5.1.18)	256	2.00e-68
			DAA00071.1	TPA: glutathione transferase A5	256	3.00e-68
			I52381	glutathione transferase (EC 2.5.1.18)	254	9.00e-68
			XP_167100.2	similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha)	253	3.00e-67
			A56801	glutathione transferase (EC 2.5.1.18) alpha y	252	5.00e-67
			S77958	glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2 (+)) - human	248	7.00e-66
			NP_001503.1	glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-aralkyltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4	244	1.00e-64
NM_011146	Mm.3020	F:(C-HI)	NP_056953.2	peroxisome proliferative activated receptor gamma, isoform 2; PPAR-gamma;		
NP_035276.1		-2.17		peroxisome proliferator activated receptor gamma	953	0
			BAA18949.1	PPAR gamma2	939	0
			S42489	peroxisome proliferator activated receptor - human	922	0
			CAA62152.1	peroxisome proliferator activated receptor gamma	916	0
			NP_005028.3	peroxisome proliferative activated receptor gamma, isoform 1; PPAR-gamma;		
				peroxisome proliferator activated receptor gamma	914	0
			BAA23354.1	ome proliferator activated-receptor gamma	904	0
			20150106	Chain A, Crystal Structure Of The Ligand Binding Domain Of Human Ppar-Gamma In Complex With The Agonist Az 242		
NM_007395	Mm.5070	F:(C-HI)	NP_004293.1	activin A type IB receptor precursor; serine(threonine) protein kinase	511	1.00e-144
NP_031421.1		-2.16			931	0

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				O00767	Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)	596	1.00e-170
				AAH05807.1	Unknown (protein for MGC:10264)	592	1.00e-169
				CAA73998.1	stearoyl CoA desaturase	589	1.00e-168
				AAF71040.1	PRO0998	579	1.00e-165
				AAH06288.1	Unknown (protein for MGC:10270)	422	1.00e-118
				I54779	stearoyl-CoA desaturase - human (fragment)	377	1.00e-104
				CAD38567.1	hypothetical protein	216	6.00e-56
NM_007824	Mm.57029	F:(C-HI)		P22680	Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII)		
NP_031850.1		-2.14, F:(C-D) -3.09			(Cholesterol 7-alpha-hydroxylase)	865	0
				NP_000771.1	cytochrome P450, subfamily VIIA, polypeptide 1; cholesterol 7-alpha-hydroxylase; cholesterol 7 alpha-monooxygenase	861	0
				AAC95426.1	oxysterol 7alpha-hydroxylase	342	8.00e-94
				NP_004811.1	cytochrome P450, subfamily VIIB, polypeptide 1; oxysterol 7alpha-hydroxylase	342	8.00e-94
				NP_004382.1	cytochrome P450, subfamily VIIB, polypeptide 1; 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-sterol 12-alpha hydroxylase CYP8B1	298	2.00e-80
				AAC63037.1		279	7.00e-75
				AAA61350.1	CYP7	259	9.00e-69
AK002979	Mm.19588	F:(C-HI)		NP_056537.1	calcyon		
BAB22492.1	1	-2.14, F:(C-D) -2.15				336	5.00e-92
AK002979	Mm.19588	F:(C-HI)					
BAB22492.1	1	-2.14, F:(C-D) -2.15				336	5.00e-92

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			NP_064732.1	activin A type IB receptor, isoform b precursor; serine(threonine) protein kinase	849	0
			I80182	activin type I receptor SKR2, splice form 2	842	0
			NP_064733.1	activin A type IB receptor, isoform c precursor; serine(threonine) protein kinase	756	0
			I80183	activin type I receptor SKR2 splice form 3	749	0
			NP_004603.1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa); transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kD)	641	0
			XP_065712.3	similar to activin receptor-like kinase 7	593	1.00e-169
			NP_660302.1	activin receptor-like kinase 7	590	1.00e-168
			I5988007	Chain A, Cytoplasmic Domain Of Unphosphorylated Type I Tgf-Beta Receptor Crystallized Without Fkbp12		
			NP_001194.1	bone morphogenetic protein receptor, type IB; serine/threonine receptor kinase	573	1.00e-163
			AAH28383.1	e morphogenetic protein receptor, type IA	417	1.00e-116
			NP_004320.1	bone morphogenetic protein receptor, type IA precursor; activin A receptor, type II-like kinase 3	413	1.00e-115
			I80180	activin type I receptor SKR2-1	413	1.00e-115
			NP_001096.1	activin A type I receptor precursor; hydroxyalkyl-protein kinase; activin A receptor, type II-like kinase 2	404	1.00e-112
			P37023	Serine/threonine-protein kinase receptor R3 precursor (SKR3) (Activin receptor-like kinase 1) (ALK-1) (TGF-B superfamily receptor type-I) (TSR-I)	399	1.00e-111
			NP_000011.1	activin A receptor type II-like 1; Activin A receptor, type II-like kinase 1	369	1.00e-102
			I59318	activin type I receptor SKR2-2	369	1e-1-1
			I80181	activin type I receptor SKR2-3 - human	325	2.00e-88
			A42100	transforming growth factor beta receptor type IIB precursor	232	1.00e-60
			NP_005054.2	stearoyl-CoA desaturase (delta-9-desaturase)	206	1.00e-52
NM_009127	Mm.14078	F:(C-HI)				
NP_033153.1	5	-2.15, F:(C-D) -3.29, F:(HI-D) -2.71				
					597	1.00e-170

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NM_011817 NP_035947.1	Mm.9653	F:(C-HI) -2.13	BAA84543.1	gadd45-related protein	313	2.00e-85
			NP_006696.1	growth arrest and DNA-damage-inducible, gamma; GADD45-gamma; gadd-related protein, 17 kD	307	2.00e-83
			AAK00414.1	growth arrest and DNA damage inducible protein gamma	303	3.00e-82
NM_027000 NP_081276.1	Mm.41800	F:(C-HI) -2.13	XP_040267.1	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein)		
			BAA91752	(GTP-binding protein NGB)	996	0
			NP_036473.1	unnamed protein product	994	0
			AAH33784.1	G protein-binding protein CRFG; GTP-binding protein	991	0
			AAC24364.1	G protein-binding protein CRFG	982	0
			NP_000763.1	putative G-binding protein	828	0
NM_007815 NP_031841.1	Mm.20764	F:(C-HI) -2.11, F:(C-D) -2.78	NP_000763.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	725	0
			P33260	Cytochrome P450 2C18 (CYP1IC18) (P450-6B/29C)	723	0
			NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	711	0
			AAB23864.2	cytochrome P-450	710	0
			BAA00123.1	cytochrome P-450	710	0
			NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	710	0
			1506290A	cytochrome P450	706	0
			AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	706	0
			P11713	Cytochrome P450 2C10 (CYP1IC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	706	0
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	705	0

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				IS2418	cytochrome P450 - human	676	0
				P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	668	0
				AAH20596.1	Unknown (protein for MGC:22146)	667	0
				NP_000761.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	665	0
				AAA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	664	0
				S66382	cytochrome P450 2C8 - human	664	0
				AAB35292.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	664	0
				AAA52161.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	660	0
				AAA52159.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	598	1.00e-170
AK006487	Mm.27196	F:(C-HI)		NP_620134.1	hypothetical protein BC015148	445	1.00e-125
BAB24612.1		-2.1					
NM_008587	Mm.4582	F:(C-HI)		AAG33129.1	MER receptor tyrosine kinase	1550	0
NP_032613.1		-2.1		NP_006334.1	c-mer proto-oncogene tyrosine kinase	1548	0
				B41527	transforming protein (axl(-)) - human	620	1.00e-177
				NP_001690.2	AXL receptor tyrosine kinase isoform 2; AXL transforming sequence/gene; oncogene AXL	619	1.00e-177
				AAH32229.1	Unknown (protein for MGC:34202)	619	1.00e-177
				NP_068713.2	AXL receptor tyrosine kinase isoform 1; AXL transforming sequence/gene; oncogene AXL	619	1.00e-177
				P30530	Tyrosine-protein kinase receptor UFO precursor (AXL oncogene)	619	1.00e-177
				CAA40338.1	unnamed protein product	619	1.00e-176
				Q06418	Tyrosine-protein kinase receptor TYRO3 precursor (Tyrosine-protein kinase RSE) (Tyrosine-protein kinase SKY) (Tyrosine-protein kinase DTK) (Protein-tyrosine kinase byk)	601	1.00e-171

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			NP_006284.1	TYRO3 protein tyrosine kinase; Brl; Dtk; Sky; Tlf; Tyro3 protein tyrosine kinase (sea-related receptor tyrosine kinase)	600	1.00e-171
			BAA21781.1	protein-tyrosine kinase	595	1.00e-169
			I38412	receptor tyrosine kinase - human	502	1.00e-141
			A56379	ZP3 receptor precursor - human	415	1.00e-118
			AAH29925.1	Similar to TYRO3 protein tyrosine kinase	417	1.00e-116
			CAA51396.1	TYRO3	364	1.00e-100
NM_007912	Mm.8534	F:(C-HI)	P00533	Epidermal growth factor receptor precursor (Receptor protein-tyrosine kinase ErbB-1)		
NP_031938.1		-2.09, F:(C-D)			1160	0
		-2.69			1160	0
			AAA52371.1	aberrant epidermal growth factor receptor		
			NP_005219.1	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian); epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Epidermal growth factor receptor	1157	0
			AAG35786.1	p110 epidermal growth factor receptor	1141	0
			AAG35790.1	truncated epidermal growth factor receptor	1141	0
			CAA25282.1	EGF (1 is 2nd base in codon)	942	0
			1007208A	epidermal growth factor receptor	884	0
			AAC50802.1	epidermal growth factor receptor precursor	700	0
			NP_005226.1	v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4		
			NP_001973.1	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian); Transformation gene ERBB-3; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	626	1.00e-179
			A36223	kinase-related transforming protein (erbB3) (EC 2.7.1.-) precursor - human	603	1.00e-172
			P21860	Receptor protein-tyrosine kinase erbB-3 precursor (c-erbB3) (Tyrosine kinase-type cell surface receptor HER3)	602	1.00e-172
			22219397	Chain A, Structure Of The Her3 (ErbB3) Extracellular Domain	602	1.00e-172

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			P04626	Receptor protein-tyrosine kinase erbB-2 precursor (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell surface receptor HER2) (MLN 19)	569	1.00e-162
			NP_004439.1	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog; Avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 2; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)	569	1.00e-162
			AAH02706.1	Similar to v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3	292	2.00e-78
			AAD56009.2	herstatin	283	9.00e-76
NM_010145 NP_034275.1	Mm.9075 F:(C-HI) -2.09, F:(C-D) -2.09		AAC41694.1	microsomal epoxide hydrolase		
			NP_000111.1	epoxide hydrolase 1, microsomal (xenobiotic); Epoxide hydroxylase 1, microsomal (xenobiotic)	818	0
			AAA52389.1	epoxide hydrolase	816	0
			CAA68486.1	precursor polypeptide (AA -20 to 435)	811	0
			AAA59580.1	microsomal epoxide hydrolase (EC 3.3.2.3).	585	1.00e-167
NM_009676 NP_033806.1	Mm.26787 F:(C-HI) -2.08		BAB40305.1	aldehyde oxidase	2204	0
			Q06278	Aldehyde oxidase	2174	0
			NP_001150.2	aldehyde oxidase 1	2171	0
			P47989	Xanthine dehydrogenase/oxidase [Includes: Xanthine dehydrogenase (XD); Xanthine oxidase (XO) (Xanthine oxidoreductase)]	1262	0
			AAA75287.1	xanthine dehydrogenase	1261	0
			NP_000370.1	xanthine dehydrogenase; xanthine oxidase; xanthine dehydrogenase	1255	0
			XP_002472.7	similar to Xanthine dehydrogenase/oxidase	915	0
			XP_172060.1	similar to ALDEHYDE OXIDASE HOMOLOG-1~data source:SPTR, source key:Q9ESH4, evidence:ISS-putative	838	0

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NM_010012	Mm.20889	F:(C-H)	NP_004382.1	cytochrome P450, subfamily VIIIb, polypeptide 1; 7		
NP_034142.1		-2.08		alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-hydroxylase	711	0
			AAC63037.1	sterol 12-alpha hydroxylase CYP8B1	679	0
			AAG31784.1	prostacyclin synthase	334	2.00e-91
			BAA28219.1	prostacyclin synthase	332	9.00e-91
			NP_000952.1	prostaglandin I2 (prostacyclin) synthase	332	9.00e-91
			BAA11910.1	prostacyclin synthase	332	9.00e-91
			AAG31785.1	prostacyclin synthase	330	4.00e-90
			AAG31783.1	prostacyclin synthase	328	1.00e-89
NM_011921	Mm.14609	F:(C-H)	AAC51652.1	aldehyde dehydrogenase 1		
NP_036051.1		-2.08			830	0
			NP_000680.2	aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1	830	0
			NP_003879.1	aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2	708	0
			O94788	Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)	706	0
			NP_000684.1	aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6	682	0
			XP_007012.1	similar to Aldehyde dehydrogenase, mitochondrial precursor (ALDH class 2) (ALDH1) (ALDH-E2)	657	0
			AAA51693.1	aldehyde dehydrogenase	656	0
			6137677	Chain A, Human Mitochondrial Aldehyde Dehydrogenase Complexed With Nad+ And Mn2+	654	0
			NP_000681.1	aldehyde dehydrogenase 2 family (mitochondrial); aldehyde dehydrogenase 2, mitochondrial	652	0
			CAA68290.1	precursor polypeptide (AA -36 to 479)	649	0
			A40872	aldehyde dehydrogenase (NAD) (EC 1.2.1.3) 5 precursor, mitochondrial	645	0
			NP_000683.2	aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5	645	0
			CAD13246.1	ba113O24.2 (aldehyde dehydrogenase 1 family, member B1 (ALDH5 ALDHX))	645	0

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			P30837	Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)	642	0
			BAA34786.1	RALDH2-T	635	0
			AAH30589.1	Similar to aldehyde dehydrogenase 1 family, member A2	622	1.00e-178
			I39431	aldehyde dehydrogenase 1 - human (fragment)	604	1.00e-172
			AAB59500.1	aldehyde dehydrogenase 2 (EC 1.2.1.3)	543	1.00e-154
			NP_036322.2	formyltetrahydrofolate dehydrogenase isoform a	447	1.00e-125
			O75891	10-formyltetrahydrofolate dehydrogenase (10-FTHFDH)	444	1.00e-124
			XP_090294.1	similar to 10-formyltetrahydrofolate dehydrogenase	431	1.00e-120
NM_018776	Mm.33962	F:(C-HI)	AAD02422.1	cytokine receptor related protein 4		
NP_061246.1		-2.07, F:(C-D) -2.11			793	0
			AAH23567.1	cytokine receptor-like factor 3	787	0
			NP_057070.1	cytokine receptor-like molecule 9	786	0
			XP_065910.1	similar to cytokine receptor-like molecule 9	293	1.00e-78
NM_007474	Mm.9970	F:(C-HI)	NP_001160.1	aquaporin 8		
NP_031500.1		-2.07			354	2.00e-97
			AAF19050.1	aquaporin 8	353	5.00e-97
NM_023737	Mm.28100	F:(C-HI)	NP_001957.1	enoyl-Coenzyme A hydratase/3-hydroxyacyl Coenzyme A dehydrogenase		
NP_076226.1		-2.07			474	1.00e-133
			AAB19482.1	3-hydroxyacyl-CoA dehydrogenase; peroxisomal enoyl-CoA hydratase	366	1.00e-101
AK005535	Mm.29483	F:(C-HI)	NP_570901.1	solute carrier family 39 (zinc transporter), member 4		
BAB24106.1		-2.06, F:(C-D) -2.16			700	0
			NP_060237.1	solute carrier family 39 (zinc transporter), member 4	578	1.00e-172
NM_009864	Mm.35605	F:(C-HI)	CAA79356.1	E-cadherin		
NP_033994.1		-2.05			1253	0

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			NP_004351.1	cadherin 1, type 1 preproprotein; calcium-dependent adhesion protein, epithelial;		
			BAA88957.1	cadherin 1, E-cadherin (epithelial); uvomorulin; cell-CAM 120/80; Arc-1	1249	0
			CAA84586.1	E-cadherin	1238	0
			AAA61259.1	E-cadherin	1179	0
			BAA88956.1	uvomorulin	1151	0
			P22223	E-cadherin	981	0
			NP_001784.2	Cadherin-3 precursor (Placental-cadherin) (P-cadherin)	749	0
			P19022	cadherin 3, type 1 preproprotein; P-cadherin; placental cadherin; cadherin 3, P-cadherin (placental); calcium-dependent adhesion protein, placental	746	0
			NP_001783.2	Neural-cadherin precursor (N-cadherin) (Cadherin-2)	581	1.00e-165
			AAB22854.1	cadherin 2, type 1 preproprotein; N-cadherin 1; cadherin 2, N-cadherin (neuronal); neural cadherin; calcium-dependent adhesion protein, neuronal	581	1.00e-165
			IJHUCN	N-cadherin	581	1.00e-165
			AAH36470.1	cadherin 2 precursor - human	579	1.00e-164
			NP_001785.2	cadherin 2, type 1, N-cadherin (neuronal)	574	1.00e-163
			P55283	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-cadherin; retinal cadherin	556	1.00e-158
			AAA03236.1	Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-CAD)	540	1.00e-153
			CAA40773.1	N-cadherin	539	1.00e-152
			BAC03677.1	unnamed protein product	526	1.00e-148
			BAB91363.1	chaperone-ABC1-like	523	1.00e-147
NM_023341	Mm.28337	F:(C-HI)				
NP_075830.1		-2.05			702	0
			BAC11143.1	unnamed protein product	700	0
			NP_064632.1	chaperone, ABC1 activity of bc1 complex like	700	0
			AAH13114.2	Similar to RIKEN cDNA 0610012P18 gene	451	1.00e-150
			NP_079152.2	hypothetical protein FLJ12229	449	1.00e-125
			AAH27473.1	Unknown (protein for MGC:36739)	440	1.00e-123
			AAG17245.1	unknown	312	2.00e-84

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AF071068	Mm.12906	F:(C-HI)	NP_000781.1	dopa decarboxylase (aromatic L-amino acid decarboxylase); aromatic L-amino acid decarboxylase		
AAC25566.1		-2.04, F:(C-D) -2.29				
			AAD40482.1	aromatic decarboxylase	878	0
			P19113	Histidine decarboxylase (HDC)	876	0
NM_009263	Mm.321	F:(C-HI)	NP_002103.1	histidine decarboxylase	525	1.00e-149
NP_033289.1		-2.04	BAC11635.1	unnamed protein product	525	1.00e-149
			P10451	Osteopontin precursor (Bone sialoprotein 1) (Urinary stone protein) (Secreted phosphoprotein 1) (SPP-1) (Nephropontin) (Uropontin)	305	2.00e-82
			I56986	OPN-a - human (fragment)	302	8.00e-82
			NP_000573.1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1); Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)	298	2.00e-80
			I76601	OPN-b - human	276	8.00e-74
			I76602	OPN-c - human (fragment)	270	4.00e-72
NM_053200	Mm.12080	F:(C-HI)	NP_036254.1	carboxylesterase 3; brain carboxylesterase BR3	248	2.00e-65
NP_444430.1	7	-2.04				
			BAB85656.1	brain carboxylesterase hBr2	1092	0
			AAH12418.1	Unknown (protein for MGC:9220)	909	0
			NP_001257.3	carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver	908	0
				carboxylesterase; carboxylesterase 2 (liver)		
			BAA04650.1	carboxylesterase	905	0
			I61085	carboxylesterase - human	904	0
			AAD53175.1	egasyn	903	0
			P23141	Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)	902	0
				acyl coenzyme A:cholesterol acyltransferase	902	0
			AAC60631.2	carboxylesterase - human	897	0
			A48809		894	0

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			I57004		carboxylesterase - human (fragment).	816	0
			CAA37147.1		serine esterase N-terminal truncated (503 AA)	812	0
			AAA83932.1		carboxylesterase	689	0
			BAA84995.1		brain carboxylesterase hBr1	672	0
AK007964	Mm.21754	F:(C-HI) -2.03, F:(C-D) -2.36	AAH20819.1		cholinephosphotransferase 1		
BAB25375.1						604	0
			NP_064629.1		choline phosphotransferase 1; cholinephosphotransferase 1;	601	0
					cholinephosphotransferase 1 alpha		
			NP_006081.1		choline/ethanolaminephosphotransferase	451	1.00e-130
			AAL39005.1		MSTP022	421	1.00e-117
			AAD44019.1		AAPT1-like protein	393	1.00e-109
			AAF87948.1		cholinephosphotransferase 1 beta	320	3.00e-98
			AAF61194.1		PRO1101	283	4.00e-80
NM_009748	Mm.23564	F:(C-HI) -2.03, F:(C-D) -2.15	NP_005859.1		Golgi vesicular membrane trafficking protein p18; Bet1 (S. cerevisiae) homolog;		
NP_033878.1					Bet1p homolog	194	4.00e-50
NM_019811	Mm.22719	F:(C-HI) -2.03, F:(C-D) -2.11	NP_061147.1		acetyl-CoA synthetase isoform a; cytoplasmic acetyl-coenzyme A synthetase;		
NP_062785.1					acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase	1314	0
			AAH12172.1		Similar to acetyl-CoA synthetase	1312	0
			BAC03849.1		unnamed protein product	1302	0
			NP_644803.1		acetyl-CoA synthetase isoform b; cytoplasmic acetyl-coenzyme A synthetase;		
					acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase	1137	0
			AAH10141.1		Unknown (protein for MGC:19474)	825	0

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				BAB14127.1	unnamed protein product	824	0
				CAB61786.2	dJ18C9.1.1 (similar to acetyl-coenzyme A synthetase, isoform 1)	701	0
				CAB93422.4	dJ1161H23.1 (similar to acetyl-coenzyme A synthetase)	673	0
				CAC33037.2	dJ18C9.1.2 (similar to acetyl-coenzyme A synthetase, isoform 2)	525	0
				CAB75500.1	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	421	1.00e-148
				XP_042770.2	similar to dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	410	1.00e-117
				BAC03853.1	unnamed protein product	404	1.00e-112
				BAB47475.1	KIAA1846 protein	335	2.00e-91
				NP_078836.1	hypothetical protein FLJ21963	325	3.00e-88
				CAC33039.2	dJ18C9.1.3 (similar to acetyl-coenzyme A synthetase, isoform 3)	218	4.00e-56
NM_011834	Mm.35020	F:(C-HI)		NP_057312.1	L-kynurenine/alpha-aminoacidate aminotransferase; kynurenine aminotransferase II	669	0
NP_035964.1		-2.03					
				AAH31068.1	Similar to L-kynurenine/alpha-aminoacidate aminotransferase	661	0
NM_009221	Mm.17484	F:(C-HI)		NP_000336.1	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor	201	2.00e-51
NP_033247.1		-2.02				197	3.00e-50
				AAC02114.1	NACP/alpha-synuclein		
NM_011125	Mm.6105	F:(C-HI)		AAH19847.1	phospholipid transfer protein	744	0
NP_035255.1		-2.01					
				NP_006218.1	phospholipid transfer protein	744	0
				CAC36020.1	dJ337O18.1.2 (Phospholipid Transfer Protein (Lipid Transfer Protein II) (isoform 2))	634	0
				AAH05045.1	Similar to phospholipid transfer protein	633	0
NM_010062	Mm.41853	F:(C-HI)		NP_001366.1	deoxyribonuclease II, lysosomal; DNase II, lysosomal		
NP_034192.1		-2.00, F:(C-D)					
		-2.4				520	1.00e-147
				T45071	hypothetical protein R31240_2 [imported]	494	1.00e-139

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			NP_067056.1	deoxyribonuclease II beta, isoform 1 precursor; DNase II-like acid DNase; endonuclease DLAD	227	5.00e-59
			AAL34449.1	endonuclease DLAD	227	5.00e-59
NM_007811	Mm.42230	F:(C-HI)	NP_000774.2	cytochrome P450, subfamily XXVIA, polypeptide 1, isoform 1; P450, retinoic acid-inactivating, 1; retinoic acid-metabolizing cytochrome; retinoic acid 4-hydroxylase		
NP_031837.1		-17.03, F:(C-D) -3.81			901	0
			O43174	Cytochrome P450 26 (Retinoic acid-metabolizing cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase)	896	0
			NP_476498.1	cytochrome P450, subfamily XXVIA, polypeptide 1, isoform 2; P450, retinoic acid-inactivating, 1; retinoic acid-metabolizing cytochrome; retinoic acid 4-hydroxylase	813	0
			NP_063938.1	cytochrome P450 retinoid metabolizing protein	391	e-108
NM_053215	Mm.16036	F:(C-HI)	NP_001068.1	UDP glucosyltransferase 2 family, polypeptide B17; UDP-glucuronyltransferase, family 2, beta-17		
NP_444445.1	2	-1.98, F:(C-D) -3.23			728	0
			XP_011097.5	similar to UDP-glucuronosyltransferase 2B15 precursor, microsomal (UDPGT) (UDPGTH-3) (HLUG4)	715	0
			NP_001067.1	UDP glucosyltransferase 2 family, polypeptide B15; UDP-glucuronyltransferase, family 2, beta-15	715	0
			AAD55093.1	UDP-glucuronosyltransferase 2B15	712	0
			XP_050345.4	similar to UDP-glucuronosyltransferase 2B4 precursor, microsomal (UDPGT) (Hydroxycholeic acid) (HLUG25) (UDPGTH-1)	705	0
			AAC95002.1	UDP-glucuronosyltransferase 2B4 precursor.	703	0
			JN0619	glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human	702	0
			AAC32272.1	UDP glucuronosyltransferase 2B4 precursor	697	0
			NP_001065.1	UDP glucosyltransferase 2 family, polypeptide B7; UDP-glucuronyltransferase, family 2, beta-7	692	0
			SI1309	glucuronosyltransferase (EC 2.4.1.17) - human	691	0

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			AAH30974.1	UDP glycosyltransferase 2 family, polypeptide B7	690	0
			NP_066962.1	UDP glycosyltransferase 2 family, polypeptide B4; UDP-glucuronosyltransferase, family 2, beta-4	688	0
			NP_001064.1	UDP glycosyltransferase 2 family, polypeptide B11	677	0
			JE0200	orphan UDP-glucuronosyltransferase (EC 2.4.-.-)	677	0
			NP_001066.1	UDP glycosyltransferase 2 family, polypeptide B10	660	0
			NP_444267.1	UDP glycosyltransferase 2 family, polypeptide B28	660	0
			NP_006789.1	UDP glycosyltransferase 2 family, polypeptide A1; UDP-glucuronosyltransferase 2 family, polypeptide A1	579	1.00e-165
NM_022411			NP_003975.1	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2; sodium-coupled citrate transporter		
NP_071856.1	Mm.57258	F:(C-D)-5.56			796	0
			AAN86530.1	Na+-coupled citrate transporter protein	531	1.00e-150
			AAF73251.1	sodium-dependent high-affinity dicarboxylate transporter	453	1.00e-127
			Q8WWT9	Solute carrier family 13, member 3 (Sodium-dependent high-affinity dicarboxylate transporter 2) (Na(+)/dicarboxylate cotransporter 3) (NaDC-3) (hNaDC3).	450	1.00e-126
			AAH35966.1	similar to solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	450	1.00e-126
			BAB71262.1	unnamed protein product	449	1.00e-126
			CAC18857.1	dJ257E24.2.1 (sodium-dependent high-affinity dicarboxylate transporter (NADC3, SDCT2) (isoform 1))	448	1.00e-125
			NP_071889.2	solute carrier family 13 (sodium/sulfate symporters), member 1; solute carrier family 13 (sodium/sulphate symporters), member 1	429	1.00e-120
			BAB15477.1	unnamed protein product	427	1.00e-119
			BAC04834.1	unnamed protein product	409	1.00e-113
			AAH30689.1	similar to solute carrier family 13	387	1.00e-107
			Q9UKG4	Solute carrier family 13, member 4 (Na+/sulfate cotransporter SUT-1).	385	1.00e-106
			CAD34590.1	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	226	7.00e-59

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NM_018866						chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant); B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1); small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-cell chemoattractant)	97	3.00e-20
NP_061354.1	Mm.10116	F:(C-D)- 3.52	NP_006410.1					
NM_009270								
NP_033296.1	Mm.22663	F:(C-D)- 3.44	AAD10823			squalene epoxidase	871	0
			NP_003120			squalene monooxygenase	857	0
			BAA11209			squalene epoxidase	589	1.00e-168
NM_017379			NP_061816.1			tubulin, alpha-like 2; tubulin, alpha 8		
NP_059075.1	Mm.32884	F:(C-D)- 3.1					867	0
			NP_005992.1			tubulin, alpha 2 isoform 1	808	0
			AAC39578.1			alpha tubulin	806	0
			NP_116093.1			tubulin alpha 6	804	0
			NP_006000.2			tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tub2	804	0
			P05209			Tubulin alpha-1 chain (Alpha-tubulin 1).	804	0
			NP_005991.1			tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain	800	0
			NP_006073.1			tubulin, alpha, ubiquitous	799	0
			CAA30026.1			alpha-tubulin	798	0
			CAA25855.1			alpha-tubulin	796	0
			XP_053177.4			similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7)	793	0
			NP_524575.1			tubulin, alpha 2 isoform 2	723	0
			NP_079079.1			hypothetical protein FLJ21665	662	0
			XP_084610.2			similar to tubulin alpha-1 chain - Chinese hamster	616	1.00e-176
			AAA91575.1			alpha-tubulin	609	1.00e-174
			AAD33872.1			alpha-tubulin	591	1.00e-169
			AAH21564.1			Similar to tubulin alpha 2	427	1.00e-119
			AAH01805.1			Unknown (protein for IMAGE:3543670)	371	1.00e-102

			XP_212565.1	similar to tubulin, beta 5	347	3.00e-95
			AAH20946.1	Beta 5-tubulin	346	4.00e-95
			P04350	Tubulin beta-5 chain (Tubulin 5 beta).	344	1.00e-94
			NP_115914.1	tubulin beta-5	344	1.00e-94
			AAH03021.1	Unknown (protein for IMAGE:2823044)	344	2.00e-94
			BAB14016.1	unnamed protein product	344	2.00e-94
			AAH29529.1	tubulin, beta, 2	343	4.00e-94
			NP_006079.1	tubulin, beta, 2	343	4.00e-94
			P07437	Tubulin beta-1 chain	343	4.00e-94
			NP_006078.2	tubulin, beta, 5	342	6.00e-94
			Q13509	Tubulin beta-4 chain (Tubulin beta-III).	342	7.00e-94
			AAH24038.1	Similar to tubulin, beta, 2	342	7.00e-94
			NP_006077.1	tubulin, beta, 4	341	1.00e-93
			NP_001060.1	tubulin, beta polypeptide	341	2.00e-93
			T08726	tubulin beta chain - human	341	2.00e-93
			AAN87335.1	class IVb beta tubulin	341	2.00e-93
			AAN85571.1	class II beta tubulin isotype	340	2.00e-93
			AAH01352.1	Tubulin, beta polypeptide paralog	340	3.00e-93
			XP_047083.4	similar to tubulin beta	338	8.00e-93
			AAL32434.1	beta-tubulin 4Q	337	2.00e-92
			I38369	beta-tubulin - human (fragment)	335	7.00e-92
			NP_110400.1	beta tubulin 1, class VI	332	1.00e-90
			O805287A	tubulin beta	330	3.00e-90
			O808321A	tubulin beta	325	7.00e-89
			AAH20171.1	Unknown (protein for MGC:1707)	325	7.00e-89
			NP_079295.1	hypothetical protein FLJ13940	306	4.00e-87
			AAH01678.1	Unknown (protein for IMAGE:2821278)	316	4.00e-86
			Q99867	Tubulin beta-4q chain	315	1.00e-85
			AAB48456.1	beta-tubulin	313	5.00e-85
			XP_170637.2	similar to beta-tubulin 4Q	268	1.00e-71

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			AAH33064.1	TUBA6 protein		265	1.00e-70
			AAB88188.1	similar to beta tubulin		259	6.00e-69
			AAH01896.1	Similar to tubulin, beta 5		259	8.00e-69
			XP_209082.1	similar to beta-tubulin 4Q		257	2.00e-68
			XP_209955.1	similar to beta-tubulin 4Q		250	3.00e-66
			CAB43252.1	hypothetical protein		239	9.00e-63
			NP_057346.1	tubulin, epsilon 1; epsilon-tubulin		212	9.00e-55
			AAH31101.1	Epsilon-tubulin		211	1.00e-54
			AAH15889.1	Similar to tubulin, beta 5		211	2.00e-54
			P23258	Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex component 1)			
			NP_057521.1	tubulin, gamma 2	208	2.00e-53	
			UBHUG	tubulin gamma chain - human	206	8.00e-53	
					205	1.00e-52	
		F:(C-D)- 2.8					
AK005060							
P29758	Mm.29125	F:(C-HI)- 2.6	AAH22526	Similar to alanine-glyoxylate aminotransferase 2-like 1	858	0	
			NP_112569	alanine-glyoxylate aminotransferase 2-like 1	836	0	
			NP_699204	hypothetical protein MGC45484	620	1.00e-177	
			NP_114106	alanine-glyoxylate aminotransferase 2 precursor, beta-alanine-pyruvate aminotransferase; beta-ALAAAT II			
			NP_116310	hypothetical protein MGC15875	273	7.00e-73	
					218	4.00e-56	
NM_021475							
		F:(C-D)- 2.74					
NP_067450.1	Mm.36742		NP_055294	disintegrin protease; ADAM-like protein decysin 1	588	1.00e-168	
			NP_068547	a disintegrin and metalloproteinase domain 28 isoform 3 preproprotein	319	9.00e-87	
			NP_055080	a disintegrin and metalloproteinase domain 28 isoform 1 preproprotein	319	9.00e-87	
			NP_068548	a disintegrin and metalloproteinase domain 28 isoform 2 preproprotein	319	9.00e-87	

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				Q9H2U9	ADAM 7 precursor (A disintegrin and metalloproteinase domain 7) (Sperm maturation-related glycoprotein GP-83).	265	2.00e-70
				NP_001100	a disintegrin and metalloproteinase domain 8 precursor	226	1.00e-58
				AAM49575	disintegrin/metalloproteinase domain 9 short protein precursor	213	1.00e-54
				NP_003807	a disintegrin and metalloproteinase domain 9 preproprotein; meltrin gamma	213	1.00e-54
				NP_694882	a disintegrin and metalloproteinase domain 33 isoform beta preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloproteinase disintegrin	196	9.00e-50
				NP_079496	a disintegrin and metalloproteinase domain 33 isoform alpha preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloproteinase disintegrin	196	9.00e-50
				AAM80482	a disintegrin and metalloproteinase domain 33	196	9.00e-50
NM_007703							
NP_031729.1	Mm.21806	F:(C-D)- 2.71		NP_689523	elongation of very long chain fatty acids like 3	387	1.00e-107
				AAG17875	CIG30	350	3.00e-96
				NP_076995	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast); long-chain fatty-acyl elongase	234	2.00e-61
				BAC11225	unnamed protein product	232	1.00e-60
NM_013878							
NP_038906.1	Mm.46268	F:(C-D)- 2.63		NP_057450	calcium binding protein 2 isoform 1; CaBP2	359	3.00e-99
				NP_112481	calcium binding protein 2 isoform 2; CaBP2	286	2.00e-77
				NP_112482	calcium binding protein 1 isoform 1; calbrain; calcium binding protein 5; calcium binding protein 1; calbrain	256	4.00e-68
				AAH15006	Similar to calcium binding protein 1 (calbrain)	253	3.00e-67
				AAH30201	Similar to calcium binding protein 1	234	1.00e-61
				NP_004267	calcium binding protein 1 isoform 2; calbrain; calcium binding protein 5; calcium binding protein 1; calbrain	233	3.00e-61
				NP_062829	calcium binding protein 5	224	1.00e-58

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				AH33167	Unknown (protein for MGC:45795)	211	9.00e-55
				NP_660201	calcium binding protein 4	211	9.00e-55
NM_011087				NP_077294.1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 6; immunoglobulin-like transcript 8		
NP_035217.1	Mm.19346 F:(C-D)-2.49					407	1.00e-113
				AAC51892.1	immunoglobulin-like transcript 5 protein	400	1.00e-111
				AAC51902.1	immunoglobulin-like transcript 5	400	1.00e-111
				AAC51893.1	immunoglobulin-like transcript 5 protein	400	1.00e-111
				AAB88120.1	immunoglobulin-like transcript 5; ILT5	399	1.00e-110
				AAB87667.1	leucocyte immunoglobulin-like receptor-3; LIR-3	399	1.00e-110
				AAC51888.1	immunoglobulin-like transcript 5 protein	399	1.00e-110
				AAC51894.1	immunoglobulin-like transcript 5 protein	399	1.00e-110
				AAC51889.1	immunoglobulin-like transcript 5 protein	399	1.00e-110
				AAC51895.1	immunoglobulin-like transcript 5 protein	399	1.00e-110
				AAC51901.1	immunoglobulin-like transcript 5	397	1.00e-110
				NP_006855.1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3; leukocyte immunoglobulin-like receptor 3	396	1.00e-109
				AAC51896.1	immunoglobulin-like transcript 5 protein	396	1.00e-109
				AAC51890.1	immunoglobulin-like transcript 5 protein	395	1.00e-109
				AAC51891.1	immunoglobulin-like transcript 5 protein	395	1.00e-109
				AAC51900.1	immunoglobulin-like transcript 5	394	1.00e-109
				AAC51897.1	immunoglobulin-like transcript 5 protein	394	1.00e-109
				AAC51887.1	immunoglobulin-like transcript 5 protein	393	1.00e-109
				AAD02203.1	immunoglobulin-like transcript 7; ILT7	393	1.00e-108
				AAL36993.1	immunoglobulin-like transcript-7	382	1.00e-105
				AAC51178.1	immunoglobulin-like transcript 1c	382	1.00e-105
				AAD50364.1	immunoglobulin-like transcript 1c	382	1.00e-105
				AAD17990.1	immunoglobulin-like transcript 1c variant 3	380	1.00e-105
				AAD50365.1	immunoglobulin-like transcript 1c	380	1.00e-105

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			AAD17991.1	immunoglobulin-like transcript 1c variant 4	380	1.00e-105
			AAC51176.1	immunoglobulin-like transcript 1a	376	1.00e-104
			JC5897	killer cell inhibitory receptor p91 precursor	376	1.00e-104
			NP_006854.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1;		
				leukocyte immunoglobulin-like receptor 6	375	1.00e-103
			NP_006857.1	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2;		
				leukocyte immunoglobulin-like receptor 7	375	1.00e-103
			NP_006831.1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	371	1.00e-102
			AAM18038.1	leucocyte immunoglobulin-like receptor	359	2.00e-98
			AAM18036.1	leucocyte immunoglobulin-like receptor	358	2.00e-98
			AAC51885.1	immunoglobulin-like transcript 6	358	3.00e-98
			AAB68666.1	monocyte inhibitory receptor precursor	358	3.00e-98
			AAM18040.1	leucocyte immunoglobulin-like receptor	357	8.00e-98
			AAM18041.1	leucocyte immunoglobulin-like receptor	357	8.00e-98
			AAM18035.1	leucocyte immunoglobulin-like receptor	356	1.00e-97
			AAM18037.1	leucocyte immunoglobulin-like receptor	356	1.00e-97
			AAH28208.1	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3	356	1.00e-97
			AAB87661.1	leucocyte immunoglobulin-like receptor-4; LIR-4	355	3.00e-97
			AAB68667.1	monocyte inhibitory receptor precursor	353	7.00e-97
			AAH36827.1	Unknown (protein for MGC:46153)	352	1.00e-96
			NP_005865.1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; leukocyte immunoglobulin-like receptor 2		
			AAL36990.1	leukocyte immunoglobulin-like receptor-2	352	1.00e-96
			AAC51883.1	immunoglobulin-like transcript 4	352	1.00e-96
			AAC51880.1	immunoglobulin-like transcript 2b	351	4.00e-96
			AAL36991.1	leukocyte immunoglobulin-like receptor-2	350	6.00e-96
			AAB88119.1	immunoglobulin-like transcript 4; ILT4	350	7.00e-96
			AAB67711.1	MIR-10	350	7.00e-96

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				NP_006660.1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1; leukocyte immunoglobulin-like receptor 1; CD85 antigen	349	1.00e-95
				AAC51879.1	immunoglobulin-like transcript 2a	345	2.00e-94
				AAG08984.1	leukocyte immunoglobulin-like receptor 1	345	2.00e-94
				AAB63522.1	leucocyte immunoglobulin-like receptor-1	345	2.00e-94
				AAC51881.1	immunoglobulin-like transcript 2c	345	2.00e-94
				AAL36989.1	leukocyte immunoglobulin-like receptor-1	345	2.00e-94
				AAB67710.1	MIR-7	345	2.00e-94
				AAL36988.1	leukocyte immunoglobulin-like receptor-1	345	2.00e-94
				XP_115639.1	similar to leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 6; immunoglobulin-like transcript 8	271	6.00e-72
				NP_077293.1	leukocyte immunoglobulin-like receptor, subfamily A, member 5; immunoglobulin-like transcript 10 ..	260	8.00e-69
				AAC99762.1	immunoglobulin-like transcript 10 protein	258	5.00e-68
				BAC03380.1	FLJ00275 protein	241	4.00e-63
				BAB71361.1	unnamed protein product	241	6.00e-63
				AAC51886.1	immunoglobulin-like transcript 6a	218	6.00e-56
NM_010849							
NP_034979.2	Mm.2444	F:(C-D)-2.45		BAA01374	p67 myc protein	593	1.00e-169
				NP_002458	v-myc myelocytomatosis viral oncogene homolog; Avian myelocytomatosis viral (v-myc) oncogene homolog; C-MYC; v-myc avian myelocytomatosis viral oncogene homolog	586	1.00e-167
				1001205A	c-myc gene	566	1.00e-161
				AAA88095	truncated c-myc-P64 protein	336	7.00e-92
				CAA25288	exon 2	335	1.00e-91
				AAA59884	c-myc protein	283	9.00e-76
				AAA88092	c-myc-P64 protein	275	2.00e-73

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NM_009414		F:(C-D)-	NP_004170.1	tryptophan hydroxylase 1 (tryptophan 5-monoxygenase); tryptophan hydroxylase (tryptophan 5-monoxygenase)	827	0
NP_033440.1	Mm.4421	2.42			825	0
			P17752	Tryptophan 5-hydroxylase 1 (Tryptophan 5-monoxygenase 1).	812	0
			AAA67050.1	tryptophan hydroxylase	662	0
			AAM28946.1	neuronal tryptophan hydroxylase		
			IMLWA	Chain A, Crystal Structure Of Human Tryptophan Hydroxylase With Bound 7,8-Dihydro-L-Biopterin Cofactor And Fe(II).	606	1.00e-173
			NP_000268.1	phenylalanine hydroxylase	491	1.00e-139
			AAI78816.1	phenylalanine hydroxylase	490	1.00e-138
			AAH26251.1	phenylalanine hydroxylase	489	1.00e-138
			2PAHA	Chain A, Tetrameric Human Phenylalanine Hydroxylase	436	1.00e-122
			IJ8TA	Chain A, Catalytic Domain Of Human Phenylalanine Hydroxylase Fe(II).	432	1.00e-121
			IPAH	Human Phenylalanine Hydroxylase Dimer, Residues 117 - 424.	429	1.00e-120
			IDMWA	Chain A, Crystal Structure Of Double Truncated Human Phenylalanine Hydroxylase With Bound 7,8-Dihydro-L-Biopterin.	427	1.00e-119
			I306389B	hydroxylase 2,Tyr	426	1.00e-119
			NP_000351.1	tyrosine hydroxylase	426	1.00e-119
			P07101	Tyrosine 3-monoxygenase (Tyrosine 3-hydroxylase) (TH).	426	1.00e-119
			CAA68472.1	tyrosine hydroxylase (AA 1-524)	426	1.00e-119
			I306389C	hydroxylase 3,Tyr	426	1.00e-119
			BAC04385.1	unnamed protein product	198	2.00e-50
NM_008039		F:(C-D)-				
NP_032065.1	Mm.57142	2.4	NP_001453	formyl peptide receptor-like 1; lipoxin A4 receptor (formyl peptide receptor related)	502	1.00e-142
			AAA58481	FMIP-related receptor II	501	1.00e-142
			AAA52474	N-formyl peptide receptor-like 2 protein	419	1.00e-117
			NP_002021	formyl peptide receptor-like 2	415	1.00e-116
			NP_002020	formyl peptide receptor 1	410	1.00e-114

PCT/US2004/010191

			CAD38582	hypothetical protein	347	5.00e-95	
NM_010098		F:(C-D)-					
NP_034228.1	Mm.32744	2.36	Q9H1Y3	Op sin 3 (Encephalopsin) (Panopsin).	561	1.00e-159	
			NP_055137	opsin 3 (encephalopsin, panopsin); opsin 3 (encephalopsin)	547	1.00e-155	
			AAO15717	encephalopsin splice variant 1-2-5-6	234	4.00e-61	
			NP_000595.1	fibroblast growth factor receptor 1 isoform 1 precursor; fms-related tyrosine kinase-2;	1562		0
NM_010206				heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth			
				factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase;			
NP_034336.1	Mm.3157	F:(C-D)- 2.35		tyrosylprotein kinase; hydroxyaryl-protein kinase			
			CAA36101.1	precursor polypeptide (AA -21 to 801)	1561		0
			AAA35958.1	heparin-binding growth factor receptor	1560		0
			NP_056934.2	fibroblast growth factor receptor 1 isoform 2 precursor; fms-related tyrosine kinase-2;	1555		0
				heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth			
				factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase;			
				tyrosylprotein kinase; hydroxyaryl-protein kinase			
			AAH15035.1	similar to fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer	1553		0
				syndrome)			
			AAA35835.1	FGF receptor-1 precursor	1553		0
			AAH18128.1	similar to fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer	1550		0
				syndrome)			
			NP_075599.1	fibroblast growth factor receptor 1 isoform 9 precursor; fms-related tyrosine kinase-2;	1462		0
				heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth			
				factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase;			
				tyrosylprotein kinase; hydroxyaryl-protein kinase			

			NP_075593.1	fibroblast growth factor receptor 1 isoform 3 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase	1357	0
			NP_075594.1	fibroblast growth factor receptor 1 isoform 4 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase	1350	0
			AAA35837.1	fibroblast growth factor receptor (FGFR) transmembrane form	1349	0
			AAA75007.1	basic fibroblast growth factor receptor protein	1347	0
			CAA68679.1	tyrosine kinase	1221	0
5			NP_000132.1	fibroblast growth factor receptor 2 isoform 1 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1147	0
			C40862	heparin-binding growth factor receptor variant alpha-a2	1142	0
			AAK94205.1	keratinocyte growth factor receptor 2 isoform BEK	1141	0
			NP_075597.1	fibroblast growth factor receptor 1 isoform 7 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase	1140	0
			NP_075261.1	fibroblast growth factor receptor 2 isoform 5 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1135	0
10			NP_075258.1	fibroblast growth factor receptor 2 isoform 2 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1101	0

				AA41794	keratinocyte growth factor receptor precursor	1098	0
				AAK94209.1	keratinocyte growth factor receptor 2 isoform K-sam-ITC2	1095	0
				AAK94206.1	keratinocyte growth factor receptor 2 isoform KGFR	1094	0
				NP_075417.1	fibroblast growth factor receptor 2 isoform I0 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1090	0
				NP_075418.1	fibroblast growth factor receptor 2 isoform I1 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1088	0
				AAH39243.1	Similar to fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon Syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	1082	0
				NP_075262.1	fibroblast growth factor receptor 2 isoform 6 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1073	0
				AAK94208.1	keratinocyte growth factor receptor 2 isoform K-sam-ITC3	1066	0
				NP_075419.1	fibroblast growth factor receptor 2 isoform I2 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1038	0
				NP_075264.2	fibroblast growth factor receptor 2 isoform 8 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1035	0

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			NP_075420.1	fibroblast growth factor receptor 2 isoform 13 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1032	0
			BAA89300.1	K-sam-II02	1029	0
			NP_075263.1	fibroblast growth factor receptor 2 isoform 7 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	1026	0
			BAA89296.1	K-sam-IIH1	1026	0
			BAA89297.1	K-sam-IIH2	1024	0
			BAA89301.1	K-sam-II03	1023	0
			BAA89299.1	K-sam-II01	1023	0
			BAA89298.1	K-sam-IIH3	1023	0
			NP_000133.1	fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4	969	0
			AAM22078.1	fibroblast growth factor receptor 3	969	0
			Q01742	Fibroblast growth factor receptor BFR-2 precursor	967	0
			AAA58470.1	growth factor receptor	964	0
			TVHU2F	fibroblast growth factor receptor flg-2 precursor	963	0
			A35969	heparin-binding growth factor receptor K-sam precursor	953	0
			AAM22079.1	fibroblast growth factor receptor 3	908	0
			AAD31561.1	fibroblast growth factor receptor 2 isoform IgIIIc isoform	905	0
			AAD31560.1	fibroblast growth factor receptor 2 IgIIb isoform	858	0
			P22455	Fibroblast growth factor receptor 4 precursor (FGFR-4).	844	0
			CAA74200.1	fibroblast growth factor 4	843	0
			NP_002002.2	fibroblast growth factor receptor 4 isoform 1 precursor; tyrosine kinase related to fibroblast growth factor receptor; tyrosylprotein kinase; protein-tyrosine kinase; hydroxyaryl-protein kinase	843	0
			TVHU4	fibroblast growth factor receptor 4 precursor	840	0

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NP_075252.1	fibroblast growth factor receptor 4 isoform 2 precursor; tyrosine kinase related to fibroblast growth factor receptor; tyrosylprotein kinase; protein-tyrosine kinase; hydroxyaryl-protein kinase	817	0
AAF27432.1	fibroblast growth factor receptor 4, soluble-form splice variant	816	0
BAC45037.1	isoform of FGFR2	767	0
AAK51435.1	fibroblast growth factor receptor 4 variant	738	0
NP_075259.1	fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	687	0
1FGKA	Chain A, Crystal Structure Of The Tyrosine Kinase Domain Of Fibroblast Growth Factor Receptor 1	628	e-179
NP_075254.1	fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4	620	e-177
1GJOA	Chain A, The Fgf2 Tyrosine Kinase Domain	579	e-165
AAB31749.1	fibroblast growth factor receptor subtype 1, FGFR1 {extracellular binding domain D(II)-D(III)} [human, A159 endometrial carcinoma cells, Peptide Partial, 279 aa].	472	e-132
1EVTC	Chain C, Crystal Structure Of Fgf1 In Complex With The Extracellular Ligand Binding Domain Of Fgf Receptor 1 (Fgfr1).	463	e-130
1CVSC	Chain C, Crystal Structure Of A Dimeric Fgf2-Fgfr1 Complex	461	e-129
NP_075265.1	fibroblast growth factor receptor 2 isoform 9 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase	375	e-103
NP_075595.1	fibroblast growth factor receptor 1 isoform 5 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase	365	e-100
1EV2E	Chain E, Crystal Structure Of Fgf2 In Complex With The Extracellular Ligand Binding Domain Of Fgf Receptor 2 (Fgfr2).	359	9.00e-99

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				1E00B	Chain B, Crystal Structure Of A Ternary Fgf1-Fgfr2-Heparin Complex.	359	9.00e-99
				NP_075596.1	fibroblast growth factor receptor 1 isoform 6 precursor; fms-related tyrosine kinase-2;	359	1.00e-98
					heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase;		
					tyrosylprotein kinase; hydroxyaryl-protein kinase		
				1I14E	Chain E, Crystal Structure Of Ser252tp Apert Mutant Fgf Receptor 2 (Fgfr2) In Complex With Fgf2	357	6.00e-98
				1I1LE	Chain E, Crystal Structure Of Pro253arg Apert Mutant Fgf Receptor 2 (Fgfr2) In Complex With Fgf2.	356	9.00e-98
				1D1SA	Chain A, Ligand-Binding Portion Of Fibroblast Growth Factor Receptor 2 In Complex With Fgfr1	354	4.00e-97
				AAC16450.1	vascular endothelial growth factor receptor 2	328	2.00e-89
				NP_002244.1	kinase insert domain receptor (a type III receptor tyrosine kinase); Kinase insert domain receptor	328	2.00e-89
				CAA43837.1	membrane protein	328	3.00e-89
				JC1402	protein-tyrosine kinase (EC 2.7.1.112) KDR	328	3.00e-89
				I38153	gene retll protein - human	327	6.00e-89
				CAA31408.1	ret tyrosine kinase (AA 1 - 860)	326	1.00e-88
				NP_065681.1	ret proto-oncogene isoform c; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET	326	1.00e-88
				AAH04257.1	ret proto-oncogene (multiple endocrine neoplasia MEN2A, MEN2B and medullary thyroid carcinoma 1, Hirschsprung disease)	326	1.00e-88
				NP_065680.1	ret proto-oncogene isoform b; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET	326	1.00e-88
				NP_066124.1	ret proto-oncogene isoform a; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET	326	1.00e-88
				AA36786.1	tyrosine kinase	325	1.00e-88
				AAA60266.1	RET tyrosine kinase/cAMP protein kinase A subunit RI	324	4.00e-88
				1VR2A	Chain A, Human Vascular Endothelial Growth Factor Receptor 2 (Kdr) Kinase Domain.	323	5.00e-88
				JN0291	protein-tyrosine kinase (EC 2.7.1.112) (clone lambda-ret-5)	323	5.00e-88

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			JN0290	protein-tyrosine kinase (EC 2.7.1.112) (clone lambda-ret-1)	323	5.00e-88
			B34735	protein-tyrosine kinase (EC 2.7.1.112) (ret) - human (fragment).	323	7.00e-88
			AAA36524.1	papillary thyroid carcinoma-encoded protein	323	7.00e-88
			NP_002010.1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	323	9.00e-88
			CAB46483.1	RET tyrosine kinase receptor	322	2.00e-87
			AAC16449.1	vascular endothelial growth factor receptor	322	2.00e-87
			INUNB	Chain B, Crystal Structure Analysis Of The Fgf10-Fgfr2b Complex	310	5.00e-84
			AAG17219.1	unknown	248	3.00e-65
			NP_005415.1	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains;	248	3.00e-65
			S24066	Tyrosine kinase with immunoglobulin and epidermal growth factor	244	3.00e-64
			IFVRA	protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor	242	2.00e-63
			NP_000450.1	Chain A, Tie2 Kinase Domain	242	2.00e-63
			AAH35514.1	TEK tyrosine kinase, endothelial	241	4.00e-63
			NP_075260.1	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	236	1.00e-61
				fibroblast growth factor receptor 2 isoform 4 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyl-kinase		
			AAB22215.1	insulin-like growth factor I receptor, IGF-IR [human, Peptide, 1367 aa].	233	7.00e-61
			NP_000866.1	insulin-like growth factor I receptor precursor	233	7.00e-61
			1M7NA	Chain A, Crystal Structure Of Unactivated Apo Insulin-Like Growth Factor-1 Receptor Kinase Domain	233	7.00e-61
NM_011781			NP_003804.1	a disintegrin and metalloproteinase domain 21 preproprotein	740	0
NP_035911.1	F:(C-D)- Mm.85003 2.33					
			NP_003805.2	a disintegrin and metalloproteinase domain 20 preproprotein	739	0
			O43506	ADAM 20 precursor (A disintegrin and metalloproteinase domain 20).	733	0
			NP_068552.1	a disintegrin and metalloproteinase domain 29 isoform 2 preproprotein	717	0

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5				NP_068551.1	a disintegrin and metalloproteinase domain 29 isoform 3 preproprotein	717	0
				Q9UKF5	ADAM 29 precursor (A disintegrin and metalloproteinase domain 29).	717	0
				NP_055084.2	a disintegrin and metalloproteinase domain 29 isoform 1 preproprotein	717	0
				AAF22163.1	disintegrin and metalloproteinase domain 29	715	0
				AAC52042.1	ADAM 21; testis-specific metalloprotease-like membrane protein	556	1.00e-158
				NP_003807.1	ADAM 30 precursor (A disintegrin and metalloproteinase domain 30).	474	1.00e-133
				Q9UKF2	ADAM 30 precursor (A disintegrin and metalloproteinase domain 30).	469	1.00e-132
				AAH28372.1	a disintegrin and metalloproteinase domain 30	469	1.00e-132
				AAF03781.1	metalloproteinase-disintegrin beta	469	1.00e-131
10				AAM49575.1	disintegrin/metalloproteinase domain 9 short protein precursor	422	1.00e-117
				BAA03499.2	KIAA0021 protein	420	1.00e-117
				S71949	metalloproteinase 12 (EC 3.4.24.-) precursor	391	1.00e-108
				NP_659441.1	a disintegrin and metalloprotease domain 32; hypothetical protein MGC26899	346	8.00e-95
				AAH26085.1	Similar to a disintegrin and metalloproteinase domain 18	345	1.00e-94
15				NP_003465.2	a disintegrin and metalloprotease domain 12 isoform 1 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha	328	2.00e-89
				Q9H013	ADAM 19 precursor (A disintegrin and metalloproteinase domain 19) (Meltrin beta) (Metalloprotease and disintegrin dentritic antigen marker) (MADDAM).	328	3.00e-89
				NP_150377.1	a disintegrin and metalloproteinase domain 19 isoform 2 preproprotein; meltrin beta	327	4.00e-89
				CAC20585.1	meltrin-beta/ADAM 19 homologue	327	4.00e-89
				NP_075525.2	a disintegrin and metalloproteinase domain 19 isoform 1 preproprotein; meltrin beta	327	4.00e-89
				NP_067673.1	a disintegrin and metalloprotease domain 12 isoform 2 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha	327	5.00e-89
20				AAC08703.2	meltrin-S	327	5.00e-89
				Q99965	ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)(Fertilin beta subunit) (PH-30) (PH30).	324	4.00e-88
				NP_001455.2	a disintegrin and metalloproteinase domain 2 proprotein; fertilin beta (a disintegrin and metalloproteinase domain 2); fertilin beta	323	5.00e-88
				AAC51110.1	fertilin beta	323	7.00e-88
25				AAF22162.1	disintegrin and metalloproteinase domain 19	323	9.00e-88

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	AAH34957.1	similar to fertilin beta protein	311	2.00e-84
	NP_055052.1	a disintegrin and metalloproteinase domain 18 preprotein	309	1.00e-83
	CAA67753.1	fertilin beta	309	1.00e-83
	AAM80482.1	a disintegrin and metalloproteinase domain 33	305	2.00e-82
5	NP_079496.1	a disintegrin and metalloproteinase domain 33 isoform alpha preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloproteinase disintegrin	305	2.00e-82
	CAC16509.2	dJ964F7.1 (novel disintegrin and reprolysin metalloproteinase family protein)	305	2.00e-82
	Q9H2U9	ADAM 7 precursor (A disintegrin and metalloproteinase domain 7) (Sperm maturation-related glycoprotein GP-83).	299	1.00e-80
	NP_055080.1	a disintegrin and metalloproteinase domain 28 isoform 1 preproprotein	293	6.00e-79
	NP_068548.1	a disintegrin and metalloproteinase domain 28 isoform 2 preproprotein	293	1.00e-78
10	NP_694882.1	a disintegrin and metalloproteinase domain 33 isoform beta preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloproteinase disintegrin	280	5.00e-75
	NP_001100.1	a disintegrin and metalloproteinase domain 8 precursor	263	1.00e-69
	AAH14566.1	A disintegrin and metalloproteinase domain 15 preproprotein	263	1.00e-69
	NP_003806.2	a disintegrin and metalloproteinase domain 15 preproprotein; metargidin	263	1.00e-69
	G02390	disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-)	263	1.00e-69
	AAH43207.1	Unknown (protein for IMAGE:5295041)	261	3.00e-69
15	AAC36742.1	sperm maturation-related glycoprotein GP-83	258	4.00e-68
	AAD55251.1	metalloproteinase-disintegrin ADAM22-3	254	4.00e-67
	BAA06670.1	metalloproteinase/disintegrin-like protein	254	4.00e-67
	NP_068369.1	a disintegrin and metalloproteinase domain 22 isoform 1 preprotein; MDC2 delta	254	4.00e-67
20	I65967	disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 2	254	4.00e-67
	NP_004185.1	a disintegrin and metalloproteinase domain 22 isoform 4 preprotein; MDC2 delta	254	4.00e-67
	NP_002381.2	a disintegrin and metalloproteinase domain 11 isoform 1 preproprotein; metalloproteinase-like, disintegrin-like, cysteine-rich protein	254	4.00e-67
	O75078	ADAM 11 precursor (A disintegrin and metalloproteinase domain 11) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein) (MDC).	254	4.00e-67
	NP_068368.2	a disintegrin and metalloproteinase domain 22 isoform 2 preprotein; MDC2 delta	254	4.00e-67
25	AAF73288.1	metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 delta	254	4.00e-67

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				AAF22476.2	MDC2		254	4.00e-67
				NP_057435.2	a disintegrin and metalloproteinase domain 22 isoform 3 preprotein; MDC2 delta		254	4.00e-67
				NP_068367.1	a disintegrin and metalloproteinase domain 22 isoform 5 preprotein; MDC2 delta		254	4.00e-67
				NP_003803.1	a disintegrin and metalloproteinase domain 23 preprotein		241	3.00e-63
				AAH24214.1	Unknown (protein for IMAGE:3604198)		226	1.00e-58
				AAH33132.1	Unknown (protein for IMAGE:3615066)		226	1.00e-58
				NP_068547.1	a disintegrin and metalloproteinase domain 28 isoform 3 preprotein		225	3.00e-58
				BAA06671.1	metalloproteinase/disintegrin-like protein		201	4.00e-51
				NP_067625.1	a disintegrin and metalloproteinase domain 11 isoform 2 preprotein; metalloproteinase-like, disintegrin-like, cysteine-rich protein		199	2.00e-50
							313	
	NM_011461							
	NP_035591.2	Mm.21642	F:(C-D)- 2.31	NP_689536	hypothetical protein MGC40611			4.00e-85
							2353	
	NM_009021							
	NP_033047.1	Mm.4736	F:(C-D)- 2.27	CAC20424	retinoid-acid induced protein 1		2353	0
				CAC20423	retinoid-acid induced protein 1		2256	0
				BAB47449	KIAA1820 protein		2249	0
				NP_060044	retinoic acid induced 1 isoform 1		1704	0
				CAD39127	hypothetical protein		1480	0
				NP_689469	retinoic acid induced 1 isoform 2		689	0
				CAD39144	hypothetical protein		524	1.00e-148
				T43490	hypothetical protein DKFZp434A139.1 - human		260	2.00e-68
				NP_109590	retinoic acid induced 1 isoform 3			
	NM_021468							
	NP_067443.1	Mm.42188	F:(C-D)- 2.18	NP_006368	UNC13 (C. elegans)-like; homolog of rat Munc13 (diacylglycerol-binding)		2958	0

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				BAA82984	KIAA1032 protein	1598	0
				XP_038604	similar to KIAA1032 protein	1478	0
				BAC03675	unnamed protein product	1404	0
				XP_085234	similar to Munc13-3	1328	0
5				CAD39069	hypothetical protein	915	0
	X03796	F:(C-D)-		NP_005156.1	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase	443	1.00e-125
	CAA27422.1	2.14	NULL				
				CAA30270.1	aldolase C	443	1.00e-125
10				NP_000025.1	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase	388	1.00e-108
				1ALD	Aldolase A (E.C.4.1.2.13)	386	1.00e-107
				CAA30979.1	aldolase A	380	1.00e-105
				NP_000026.1	aldolase B, fructose-bisphosphate; Aldolase B, fructose-bisphosphatase	335	4.00e-92
				P05062	Fructose-bisphosphate aldolase B (Liver-type aldolase).	335	4.00e-92
15				AAA51691.1	aldolase B	334	8.00e-92
				BAA00125.1	aldolase B	334	8.00e-92
				1QO5A	Chain A, Fructose 1,6-Bisphosphate Aldolase From Human Liver Tissue.	333	1.00e-91
				AAH29399.1	Similar to aldolase B, fructose-bisphosphate	333	1.00e-91
				1313294A	aldolase B	328	3.00e-90
				AAH00367.1	Similar to aldolase A, fructose-bisphosphate	241	9.00e-64
20				AAH16170.1	Similar to aldolase A, fructose-bisphosphate	239	2.00e-63
	NM_007489			NP_001169.2	aryl hydrocarbon receptor nuclear translocator-like	1219	0
		F:(C-D)-					
25	NP_031515.1	2.13	Mm.12177	JC5405	brain and muscle Ah receptor nuclear translocator-like protein, BMAL1b	1218	0
				AAH41129.1	Unknown (protein for MGC:47515)	1204	0
				O00327	BMAL1 protein (Brain and muscle ARNT-like 1) (Member of PAS protein 3)	1130	0
					(Basic-helix-loop-helix-PAS orphan MOP3) (BHLH-PAS protein JAP3).		
				AAC51213.1	PAS protein 3	1102	0

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				AAG34652.1	cycle-like factor CLIF		560	1.00e-159
				AAL50339.1	brain-muscle-ARNT-like transcription factor 2a		557	1.00e-158
				AAL50340.1	brain-muscle-ARNT-like transcription factor 2b		551	1.00e-156
				AAL50341.1	brain-muscle-ARNT-like transcription factor 2c		545	1.00e-154
				AAL50342.1	brain-muscle-ARNT-like transcription factor 2d		545	1.00e-154
				AAF71306.1	bHLH-PAS transcription factor MOP9		539	1.00e-153
				AAF71307.1	bHLH-PAS transcription factor MOP9		538	1.00e-152
				AAH00172.2	Similar to transcription factor BMAL2		536	1.00e-152
				BAB01485.1	transcription factor BMAL2		533	1.00e-151
				JC5407	brain and muscle Ah receptor nuclear translocator-like protein, BMAL1e		478	1.00e-134
				PC4288	brain and muscle Ah receptor nuclear translocator-like protein, BMAL1d		451	1.00e-126
				BAA19936.1	BMAL1c		350	4.00e-96
				NP_001659.1	aryl hydrocarbon receptor nuclear translocator isoform 1; dioxin receptor, nuclear translocator; hypoxia-inducible factor 1, beta subunit		328	3.00e-89
				CAD38953.1	hypothetical protein		323	1.00e-87
				Q9HBZ2	Aryl hydrocarbon receptor nuclear translocator 2 (ARNT protein 2).		318	3.00e-86
				AAH36099.1	Unknown (protein for MGC:33872)		318	3.00e-86
				NP_055677.1	aryl-hydrocarbon receptor nuclear translocator 2; aryl hydrocarbon receptor nuclear translocator 2		317	7.00e-86
				AAC03365.1	aryl hydrocarbon receptor nuclear translocator; Arnt		235	2.00e-61
NM_013533							821	0
NP_038561.1	Mm.2514	F:(C-D)- 2.13		NP_062832	protein 'A' isoform 2; protein 'A'			
				AAH07918	Similar to protein A		400	1.00e-111
				NP_055264	protein 'A' isoform 1; protein 'A'		400	1.00e-111
				AAC50467	protein A-3		269	2.00e-71

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NM_013598		F:(C-D)- 2.12	NP_000890	mast cell growth factor, isoform b, precursor		398	1.00e-110
NP_038626.1	Mm.4235		1SCFA	Chain A, Human Recombinant Stem Cell Factor		391	1.00e-108
			NP_003985	KIT ligand isoform a, precursor; mast cell growth factor; stem cell factor precursor		352	3.00e-96
			AAD22048	stem cell factor precursor		348	3.00e-95
			1EXZA	Chain A, Structure Of Stem Cell Factor		218	3.00e-56
NM_007753			NP_001861.1	mast cell carboxypeptidase A3 precursor		719	0
NP_031779.1	Mm.1135	F:(C-D)- 2.08	AAH12613.1	Mast cell carboxypeptidase A3 precursor		716	0
			AAB22578.2	mast cell carboxypeptidase A; MC-CPA		557	1.00e-158
			P15086	Carboxypeptidase B precursor (Pancreas-specific protein) (PASP).		446	1.00e-125
			CAA12163.1	procarboxypeptidase B		444	1.00e-124
			1KWMA	Chain A, Human Procarboxypeptidase B: Three-Dimensional Structure And Implications For Thrombin-Activatable Fibrinolysis Inhibitor (Tafi).		442	1.00e-124
			NP_001862.1	pancreatic carboxypeptidase B1 precursor; pancreas-specific protein		438	1.00e-123
			DAA00037.1	TPA: carboxypeptidase A-6; CPA6		358	8.00e-99
			NP_065094.2	carboxypeptidase B precursor		358	1.00e-98
			AAH07057.1	carboxypeptidase B2 (plasma)		330	2.00e-90
			NP_001863.1	plasma carboxypeptidase B2 isoform a preproprotein; carboxypeptidase U; thrombin-activatable fibrinolysis inhibitor; carboxypeptidase B-like protein; thrombin-activable fibrinolysis inhibitor		330	4.00e-90
			NP_057436.1	carboxypeptidase A4; carboxypeptidase A3		299	7.00e-81
			NP_775100.1	carboxypeptidase O		298	2.00e-80
			DAA00036.1	TPA: carboxypeptidase O; CPO		298	2.00e-80
			P48052	Carboxypeptidase A2 precursor		296	4.00e-80
			1AYE	Human Procarboxypeptidase A2		294	2.00e-79
			NP_001860.1	carboxypeptidase A2 (pancreatic)		294	2.00e-79

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			AAH07009.1	Carboxypeptidase A2 (pancreatic)	294	2.00e-79
			AAH05279.1	Pancreatic carboxypeptidase A1 precursor	293	4.00e-79
			NP_001859.1	pancreatic carboxypeptidase A1 precursor; Carboxypeptidase A	291	1.00e-78
			AAL37611.1	carboxypeptidase A5	286	6.00e-77
			AAH42996.1	Similar to carboxypeptidase A5	286	6.00e-77
			AAH39362.1	CPA5 protein	285	1.00e-76
			IDTDA	Chain A, Crystal Structure Of The Complex Between The Leech Carboxypeptidase Inhibitor And The Human Carboxypeptidase A2 (Lci-Cpa2).	267	3.00e-71
			AAM19307.1	metallocarboxypeptidase A6	240	3.00e-63
			NP_057497.2	plasma carboxypeptidase B2 isoform b; carboxypeptidase U; thrombin-activatable fibrinolysis inhibitor; carboxypeptidase B-like protein; thrombin-activatable fibrinolysis inhibitor	235	1.00e-61
			BAA90475.1	carboxypeptidase B-like protein	235	1.00e-61
			BAC04122.1	unnamed protein product	211	2.00e-54
			AAF91231.1	carboxypeptidase B precursor	200	3.00e-51
NM_019952					464	
NP_064336.1	Mm.32518	F:(C-D)- 2.07	NP_037378	cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3		1.00e-131
NM_031390					204	
NP_113567.1	Mm.10823 9	F:(C-D)- 2.07	NP_006106 AAH39731	preferentially expressed antigen in melanoma; melanoma antigen preferentially expressed in tumors; Opa-interacting protein OIP4; preferentially expressed antigen of melanoma preferentially expressed antigen in melanoma	204	5.00e-52 5.00e-52
NM_016851						
NP_058547.1	Mm.4179	F:(C-D)- 2.07	NP_006138 NP_116032 NP_002191	interferon regulatory factor 6; Popliteal pterygium syndrome interferon regulatory factor 5 isoform b interferon regulatory factor 5 isoform a	923 444 429	0 1.00e-124 1.00e-119

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					AAC50779	lymphocyte specific interferon regulatory factor/interferon regulatory factor 4	221	6.00e-57
					Q15306	Interferon regulatory factor 4 (IRF-4) (Lymphocyte specific interferon regulatory factor)	219	2.00e-56
					NP_002451	(LSIRF) (NF-EM5) (Multiple myeloma oncogene 1).	216	2.00e-55
					BAA11335	interferon regulatory factor 4; multiple myeloma oncogene 1	208	5.00e-53
					NP_002154	ICSAT transcription factor	198	4.00e-50
5						interferon consensus sequence binding protein 1; H-ICSBP; interferon regulatory factor 8		
	NM_009988							
				F:(C-D)-				
	NP_034118.1	Mm.8702	2.06		AAD31772	coxsackie and adenovirus receptor protein	611	1.00e-175
						coxsackie virus and adenovirus receptor; 46 kD coxsackievirus and adenovirus receptor		
10					NP_001329	(CAR) protein	600	1.00e-171
					AAL68880	coxsackie-adenovirus-receptor isoform CAR4/7	351	1.00e-96
					XP_208848	similar to coxsackie-adenovirus-receptor isoform CAR4/7	298	1.00e-80
					AAL68879	coxsackie-adenovirus-receptor isoform CAR3/7	254	3.00e-67
					IF5WA	Chain A, Dimeric Structure Of The Coxsackie Virus And Adenovirus Receptor D1 Domain	233	4.00e-71
						Chain B, Knob Domain From Adenovirus Serotype 12 In Complex With Domain 1 Of Its Cellular Receptor Car		
15					IKACB	Chain R, Cyro-Em Structure Of Coxsackievirus B3(M Strain) With Its Cellular Receptor,	233	7.00e-61
					IJEWR	Coxsackievirus And Adenovirus Receptor (Car).	228	2.00e-59
	NM_025436							
				F:(C-D)-				
	NP_079712.1	Mm.30119	2.04		NP_006736	sterol-C4-methyl oxidase-like; C-4 methyl sterol	578	1.00e-164
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	NM_019871							
				F:(C-D)-				
	NP_063924.1	Mm.6211	2.04		NP_689675	hypothetical protein FLJ40154	186	5.00e-88
					NP_473369	acyl-malonyl condensing enzyme	182	2.00e-85
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NM_009770		F:(C-D)- 2.02	Mm.2823		B-cell translocation gene 3; abundant in neuroepithelium area protein ANA - human	NP_006797 T09539	456	1.00e-128
NP_033900.1					Unknown (protein for MGC:8928)	AH11957	449	1.00e-126
					ANA	AAF24345	434	1.00e-121
							241	2.00e-63
NM_009993	Mm.15537	F:(C-D) -3.27			cytochrome P450	AAK25728.1	778	0
NP_034123.1					cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase	NP_000752.1	775	0
					cytochrome P450-1A2	AAF13599.1	774	0
					cytochrome P450 4	AAA35738.1	773	0
					cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	NP_000490.1	705	0
					cytochrome P-450-1	AAA52139.1	703	0
					cytochrome P(1)-450	CAG26458.1	703	0
					similar to CYTOCHROME P450 1A2 (CYPIA2) (P450-P3) (P(3)450) (P450 4)	XN_044660.4	588	1.00e-158
					cytochrome P450 CYP1B1	AAC50809.1	349	5.00e-96
					cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	NP_000095.1	349	5.00e-96
NM_007706	Mm.4132	F:(C-D) -2.51			suppressors of cytokine signaling-2; STAT induced STAT inhibitor-2;	NP_003868.1	364	1.00e-100
NP_031732.1					cytokine-inducible SH2 protein 2	JCS626	361	1.00e-100
					STAT induced STAT inhibitor 2 - human	JCS760	360	3.00e-99
					cytokine-inducible SH2 protein 2 - human			

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			BAA22536.1	CIS2		359	3.00e-99
			AAC98896.1	suppressor of cytokine signalling-2; HSSOCS-2		350	3.00e-96
NM_009396	Mm.4348	F:(C-D)	NP_006282.1	tumor necrosis factor, alpha-induced protein 2			
NP_033422.1		-2.5					
AK004924	Mm.27889	F:(C-D)	XP_058753.1	similar to coenzyme A diphosphatase	790	0	
BAB23675.1		-2.42					
NM_029813	Mm.15981	F:(C-D)	NP_689814.1	hypothetical protein FLJ38281	300	7.00e-81	
NP_084089.1	3	-2.4			373	1.00e-1	
			XP_091960.1	similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	373	1.00e-1	
			NP_066358.1	zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	364	1.00e-1	
			NP_699189.1	hypothetical protein FLJ90396	364	1.00e-1	
			XP_091958.1	similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4	364	1.00e-1	
			XP_091968.4	similar to zinc finger protein 91 (HPF7, HTF10)	353	6.00e-9	
			AAF71790.1	ZNF180	347	6.00e-9	
			NP_037388.1	zinc finger protein 180 (HHZ168)	347	6.00e-9	
			NP_003428.1	zinc finger protein 136 (clone pHZ-20)	345	1.00e-9	
			NP_689815.1	hypothetical protein FLJ40981	344	3.00e-9	
			NP_085116.1	hypothetical protein FLJ21628	343	8.00e-9	
			AAD23607.1	BC37295_1	341	2.00e-9	
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			BAC04309.1	unnamed protein product	338	2.00e-9
			BAB21801.1	KIAA1710 protein	337	3.00e-9
			XP_032812.1	similar to hypothetical protein FLJ40981	337	3.00e-9
			XP_031283.1	similar to Hypothetical zinc finger protein KIAA1710	337	3.00e-9
			P35789	Zinc finger protein 93 (Zinc finger protein HTF34)	336	8.00e-9
			NP_003427.1	zinc finger protein 135 (clone pHZ-17)	336	1.00e-9
			NP_653290.2	hypothetical protein FLJ32191	335	1.00e-9
			BAB71257.1	unnamed protein product	333	8.00e-9
			BAC04764.1	unnamed protein product	332	2.00e-9
			NP_003420.1	zinc finger protein 85 (HPF4, HTF1)	330	5.00e-9
			BAA86512.1	KIAA1198 protein	328	3.00e-8
			XP_032674.1	similar to Hypothetical zinc finger protein KIAA1198	328	3.00e-8
			NP_660338.1	similar to Zinc finger protein 136	327	4.00e-8
			BAB71272.1	unnamed protein product	327	6.00e-8
			XP_065387.2	similar to Zinc finger protein 135	326	1.00e-8

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			XP_086070.1	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	325	1.00e-8
			NP_003421.1	zinc finger protein 91 (HPF7, HTF10)	325	1.00e-8
			XP_068538.2	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	325	2.00e-8
			XP_028314.1	similar to KRAB zinc finger protein KR18	324	3.00e-8
			XP_115658.2	similar to Zinc finger protein 208	324	3.00e-8
			T14757	hypothetical protein DKFZp572C163.1 - human (fragment)	324	3.00e-8
			XP_091983.1	similar to Zinc finger protein 135	324	4.00e-8
			CAB94232.2	zinc finger protein	323	5.00e-8
			NP_003419.1	zinc finger protein 84 (HPF2)	323	5.00e-8
			B32891	finger protein 2, placental - human	323	5.00e-8
			NP_055295.1	zinc finger protein AF020591	323	7.00e-8
			AAC51180.1	kruppel-related zinc finger protein	323	9.00e-8
			XP_092097.1	similar to Zinc finger protein 93 (Zinc finger protein HTF34)	322	1.00e-8
			AAH36110.1	Similar to zinc finger protein 208	322	1.00e-8
			BAC04610.1	unnamed protein product	322	2.00e-8

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			NP_612143.1	hypothetical protein FLJ31526	322	2.00e-8
			NP_067039.1	zinc finger protein 71; endothelial zinc finger protein induced by tumor necrosis factor alpha	321	3.00e-8
			NP_003399.1	zinc finger protein 37 homolog (mouse); Zinc finger protein-37, mouse, homolog of;	321	3.00e-8
			BAC04064.1	zinc finger protein homologous to Zfp37 in mouse	321	3.00e-8
				unnamed protein product		
			Q9Y6Q3	Zinc finger protein ZFP-37	321	3.00e-8
			AAD23608.1	BC37295_2 (partial)	321	3.00e-8
			AAL58442.1	zinc finger protein 328	321	3.00e-8
			BAB47481.1	KIAA1852 protein	321	3.00e-8
			AAH37209.1	Unknown (protein for MGC:41936)	320	4.00e-8
			XP_171752.1	similar to zinc finger protein 29	320	4.00e-8
			XP_092090.2	similar to Hypothetical zinc finger protein KIAA1473	320	6.00e-8
			BAA24050.1	Zinc-finger protein	320	6.00e-8
			NP_443092.1	kruppel-like zinc finger protein	319	1.00e-8
			XP_171940.1	similar to BC37295_1	318	2.00e-8
			NP_653294.1	hypothetical protein FLJ30932	318	2.00e-8

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XP_064929.5	similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)	318	2.00e-8
NP_079009.1	hypothetical protein FLJ14345	318	2.00e-8
NP_003416.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain	318	2.00e-8
AAF63030.1	Zinc finger protein ZNF45	318	2.00e-8
NP_008889.1	zinc finger protein 16 (KOX 9)	318	2.00e-8
CAD39111.1	hypothetical protein	318	2.00e-8
XP_092093.1	similar to Zinc finger protein 85	318	2.00e-8
P17020	Zinc finger protein 16 (Zinc finger protein KOX9)	318	2.00e-8
AAH06528.1	zinc finger protein 43 (HTF6)	318	3.00e-8
XP_086128.1	similar to Zinc finger protein 35 (Zfp-35)	318	3.00e-8
XP_065116.3	similar to zinc finger protein 91 (HPF7, HTF10)	317	4.00e-8
NP_003414.1	zinc finger protein 43 (HTF6)	317	4.00e-8
AAH35579.1	Similar to zinc finger protein 208	317	4.00e-8
NP_061121.1	zinc finger protein ZFP	317	5.00e-8
NP_003442.1	zinc finger protein 177	317	5.00e-8

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XP_087503.1	similar to zinc finger protein 91 (HPF7, HTF10)	317	5.00e-8
XP_033888.3	similar to Zinc finger protein 41	317	6.00e-8
CAC88162.1	bB479F17.3 (zinc finger protein 41)	317	6.00e-8
NP_700359.1	zinc finger protein 41	317	6.00e-8
A54661	zinc finger protein ZNF41 - human (fragment)	317	6.00e-8
AAH22992.1	Unknown (protein for MGC:29879)	317	6.00e-8
XP_166367.1	similar to Zinc finger protein 184	317	6.00e-8
BAC04216.1	unnamed protein product	316	8.00e-8
NP_065704.1	zinc finger protein 287	316	8.00e-8
NP_061025.3	zinc finger protein 331; zinc finger protein 463; C2H2-like zinc finger protein	315	1.00e-8
AAF78075.1	KRAB zinc finger protein	315	1.00e-8
AAH36714.1	Unknown (protein for IMAGE:4846514)	315	2.00e-8
T12489	hypothetical protein DKFZp572P0920.1 - human (fragment)	315	2.00e-8
XP_032810.1	similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)	315	2.00e-8
AAF88107.1	Hypothetical zinc finger-like protein	315	2.00e-8

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		NP_612203.1	TRAF6-inhibitory zinc finger protein; TRAF6-binding zinc finger protein	314	3.00e-8
		XP_092088.3	similar to zinc finger protein 91 (HPF7, HTF10)	314	3.00e-8
		XP_047554.4	similar to Hypothetical zinc finger protein KIAA1473	314	4.00e-8
		NP_006620.1	zinc finger protein 271	313	5.00e-8
		Q9P255	Hypothetical zinc finger protein KIAA1473	313	9.00e-8
		BAB85542.1	KIAA1956 protein	313	9.00e-8
		XP_085836.1	similar to Hypothetical zinc finger protein KIAA1956	313	9.00e-8
		XP_047550.1	similar to Hypothetical zinc finger protein KIAA1473	313	9.00e-8
		NP_003406.1	zinc finger protein 268	312	1.00e-8
		AAH36038.1	Unknown (protein for MGC:33240)	312	1.00e-8
		AAK69307.1	ZNF268B	312	1.00e-8
		S47071	finger protein HZF3, Krueppel-related - human (fragment)	312	2.00e-8
		NP_037512.1	zinc finger protein 228	312	2.00e-8
		NP_446464.1	argininosuccinate synthetase		
NM_007494	Mm.3217	F:(C-D)		793	0
NP_031520.1		-2.36		781	0
			similar to argininosuccinate synthetase	612	1.00e-175

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			XP_167277.1	similar to argininosuccinate synthetase	602	1.00e-172
			XP_062010.1	similar to argininosuccinate synthetase	601	1.00e-172
			XP_094542.1	similar to argininosuccinate synthetase	410	1.00e-114
			XP_172419.1	similar to argininosuccinate synthetase	305	9.00e-83
			XP_095989.1	similar to argininosuccinate synthetase	253	4.00e-67
5			AA096328.1	argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	231	2.00e-60
			XP_070116.1	similar to argininosuccinate synthase (citrulline-aspartate ligase); 84% Similarity to P09034 (NID:g114291)	218	2.00e-56
			XP_070928.1	similar to argininosuccinate	211	2.00e-54
			NP_002585.2	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5	1247	0
10	NM_008792	Mm.1247		endoprotease	1244	0
	NP_032818.1	F:(C-D) -2.35		dJ531H16.1 (proprotein convertase subtilisin/kexin type 2 (NEC2))	892	0
			AAA60032.1	tubulin, beta polypeptide	838	0
			CAB89428.1	tubulin beta chain - human	835	0
			AAH01352.1	tubulin, beta polypeptide	833	0
			T08726	tubulin, beta, 2	830	0
			NP_001060.1	Similar to tubulin, beta, 2	828	0
			NP_006079.1	tubulin, beta, 2	827	0
			AAH24038.1	Tubulin beta-5 chain	823	0
			AAH29529.1	tubulin, beta 5	822	0
			P05218	tubulin, beta, 5	820	0
			AAH20946.1	Tubulin beta-1 chain	815	0
			NP_006078.2	Tubulin beta-5 chain	813	0
			P07437	tubulin beta	801	0
			P04350	beta-tubulin - human (fragment)	795	0
			0808321A	Unknown		
			I38369			
			AAH03021.1			

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			Q13509	Tubulin beta-4 chain (Tubulin beta-III)	794	0
			NP_006077.1	tubulin, beta, 4	793	0
			XP_047083.4	similar to neu differentiation factor - human (fragment)	789	0
			BAB14016.1	unnamed protein product	785	0
			NP_115914.1	similar to chicken tubulin beta 5	785	0
			AAL32434.1	beta-tubulin 4Q	775	0
			0805287A	tubulin beta	770	0
			XP_047436.3	similar to tubulin, beta 3	756	0
			NP_064424.1	tubulin, beta polypeptide 4, member Q	731	0
			AAB48456.1	beta-tubulin	726	0
			AAH01678.1	Unknown (protein for IMAGE:2821278)	708	0
			NP_110400.1	beta tubulin 1, class VI	691	0
			XP_027577.1	similar to beta-tubulin 4Q	644	0
			XP_170752.1	similar to peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein	602	1.00e-172
			P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)	600	1.00e-171
			AAH06500.1	Unknown (protein for MGC:2366)	600	1.00e-171
			NP_006812.2	peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein	599	1.00e-171
			BAA91989.1	unnamed protein product	598	1.00e-171
			NP_689544.1	hypothetical protein FLJ31235	494	1.00e-139
			AAC42007.1	ORF; putative	405	1.00e-113
			XP_090885.1	similar to Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)	280	4.00e-75
			NP_060301.1	hypothetical protein FLJ20456	254	6.00e-70
			AAH12021.1	Unknown (protein for MGC:21737)	245	5.00e-67
			NP_004419.1	ephrin A1 precursor; eph-related receptor tyrosine kinase ligand 1 (tumor necrosis factor, alpha-induced protein 4)	353	2.00e-97
			AK006569			
			BAB24656.1			
			NP_010107			
			NP_034237.1			

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				AAH32698.1	ephraim-A1		351	8.00e-97
NM_025754	Mm.20213	F:(C-D)		NP_000025.1	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase		647	0
NP_080030.1		-2.13		229674	Chain, Aldolase A (E.C.4.1.2.13)		645	0
				CAA30979.1	aldolase A		636	0
				NP_005156.1	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase		556	1.00e-158
				CAA30270.1	aldolase C		555	1.00e-158
NM_008303	Mm.19760	F:(C-D)		NP_002148.1	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1		171	3.00e+43
NP_032329.1	1	-2.12		NP_001002.1	(chaperonin 10)			
NM_011300	Mm.5281	F:(C-D)			ribosomal protein S7; 40S ribosomal protein S7.		376	1.00e-104
NP_035430.1		-2.11		AAAB00969.1	ribosomal protein		372	1.00e-103
				XP_012638.7	similar to bA271B5.1 (similar to ribosomal protein S7)		368	1.00e-102
				CAC17691.1	bA271B5.1 (similar to ribosomal protein S7)		368	1.00e-102
				XP_015717.4	similar to ribosomal protein S7		352	3.00e-97
				XP_056970.1	similar to ribosomal protein S7		341	5.00e-94
				XP_066966.1	similar to ribosomal protein S7		297	1.00e-80
				XP_068930.1	similar to ribosomal protein S7		290	2.00e-78
				XP_170827.1	similar to ribosomal protein S7		273	1.00e-73
				XP_117815.2	similar to ribosomal protein S7		236	2.00e-62
AK011896	Mm.27248	F:(C-D)		BAB14594.1	unnamed protein product			
BAB27902.1		-2.1					213	5.00e-55
				CAB66586.2	hypothetical protein		211	3.00e-54
NM_008322	Mm.2966	F:(C-D)		P48735	isocitrate dehydrogenase [NADP], mitochondrial precursor (Oxalosuccinate		850	0
NP_032348.1		-2.1		NP_002159.1	decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) (ICD-M)		845	0
					isocitrate dehydrogenase 2 (NADP+), mitochondrial; isocitrate dehydrogenase,		734	0
					mitochondrial		566	1.00e-161
				AAC50455.1	isocitrate dehydrogenase		566	1.00e-161
				XP_028869.1	similar to isocitrate dehydrogenase 1 (NADP+), soluble			
				NP_005887.1	isocitrate dehydrogenase 1 (NADP+), soluble			

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			T46280	isocitrate dehydrogenase (NADP) (EC 1.1.1.42), cytosolic [similarity]	565	1.00e-161
			XP_068996.1	similar to isocitrate dehydrogenase 1 (NADP+), soluble	436	1.00e-122
NM_011802	Mm.30088	F:(C-D)	NP_006651.2	ClpX caseinolytic protease X homolog; energy-dependent regulator of proteolysis;		
NP_035932.1		-2.08		ClpX (caseinolytic protease X, E. coli)	1041	0
			CAB66856.1	hypothetical protein	856	0
AK004138	Mm.29364	F:(C-D)	CAA36480.1	ORFII		
BAB23187.1		-2.06				
			NP_060110.1	hypothetical protein FLJ20048	125	1.00e-65
			AAC51269.1	putative p150	243	8.00e-61
			AAC51271.1	putative p150	126	5.00e-52
			AAC51276.1	putative p150	129	3.00e-51
			AAA88037.1	unknown protein	127	3.00e-51
NM_008509	Mm.1514	F:(C-D)	NP_000228.1	lipoprotein lipase precursor	127	3.00e-51
NP_032535.1		-2.05, F:(HI-D)				
		-2.42				
			AAH11353.1	Similar to lipoprotein lipase	838	0
			AAC61679.1	lipoprotein lipase precursor	836	0
			NP_006024.1	endothelial lipase precursor; endothelial cell-derived lipase	602	1.00e-170
			NP_000227.1	lipase C precursor	436	1.00e-120
			AAA59520.1	hepatic lipase precursor	380	1.00e-103
			A28997	triacylglycerol lipase (EC 3.1.1.3) precursor, hepatic	379	1.00e-103
NM_013541	Mm.426	F:(C-D)	5822569	Chain A, Crystal Structure Of Hgstp1-1[v104] Complexed With The Gsh Conjugate	379	1.00e-103
NP_038569.1		-2.05		Of (+)-Anti-Bpde	377	1.00e-1
			2554839	Chain A, Crystal Structure Of Human Glutathione S-Transferase P1-1[v104]		05
				Complexed With S-Hexylglutathione	377	1.00e-1
			AAC13869.1	glutathione S-transferase-P1c	376	04
			NP_000843.1	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester synthase III	376	1.00e-1
						04

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		4699783	Chain A, Human Glutathione S-Transferase P1-1 Y49f Mutant	375	1.00e-1
		CAA30894.1	glutathione S-transferase	374	1.00e-1
		2981694	Chain A, Glutathione S-Transferase In Complex With Glutathione	374	1.00e-1
		4139536	Chain A, Glutathione S-Transferase P1-1	374	1.00e-1
		2914230	Chain A, Human Glutathione S-Transferase P1-1 Y108f Mutant	373	1.00e-1
		23200508	Chain A, A Folding Mutant Of Human Class Pi Glutathione Transferase, Created By Mutating Glycine 146 Of The Wild-Type Protein To Alanine	372	1.00e-1
		2780951	Chain A, Glutathione S-Transferase In Complex With P-Bromobenzylglutathione	372	1.00e-1
		11514451	Chain A, Glutathione Transferase P1-1	371	1.00e-1
		23200510	Chain A, A Folding Mutant Of Human Class Pi Glutathione Transferase, Created By Mutating Glycine 146 Of The Wild-Type Protein To Valine	371	1.00e-1
		11514448	Chain A, Crystal Structure Of Pi Class Glutathione Transferase	370	1.00e-1
		A41177	glutathione transferase (EC 2.5.1.18) / fatty-acyl-ethyl-ester synthase (EC 3.1.1.67)	368	1.00e-1
		20664358	III, myocardial	360	1.00e-1
			Chain A, Crystal Structure Of A Recombinant Glutathione Transferase, Created By Replacing The Last Seven Residues Of Each Subunit Of The Human Class Pi Isoenzyme With The Additional C-Terminal Helix Of Human Class Alpha Isoenzyme		00
		A60445	glutathione transferase (EC 2.5.1.18) pi - human	309	2.00e-8
NM_008756	Mm.4807	F:(C-D)			4
NP_032782.1	-2.04	NP_002529.1	occludin	899	0

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			AAH29886.1	occludin		897	0
NM_009349	Mm.299	F:(C-D)	AAAD04723.1	thioether S-methyltransferase-like; similar to P40936 (PID:g731019)		271	8.00e-73
NP_033375.1		-2.04					
			O95050	Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase)			
				(Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)	267		2.00e-71
			NP_006765.3	indolethylamine N-methyltransferase; thioester S-methyltransferase-like	266		5.00e-71
			AAH33813.1	Unknown (protein for IMAGE:5209218)	266		5.00e-71
			NP_006160.1	nicotinamide N-methyltransferase	239		6.00e-63
NM_023850	Mm.38021	F:(C-D)	NP_003645.1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1; carbohydrate (chondroitin 6/keratan) sulfotransferase 1			
NP_076339.1		-2.03			778		0
			NP_004264.2	carbohydrate (chondroitin 6) sulfotransferase 3; chondroitin 6-sulfotransferase	305		1.00e-82
			BAA32576.1	chondroitin 6-sulfotransferase	303		7.00e-82
			NP_067628.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6; macular dystrophy, corneal, 1; carbohydrate sulfotransferase 6; corneal N-acetylglucosamine 6-sulfotransferase			
					214		4.00e-55
			NP_005760.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4; N-acetylglucosamine 6-O-sulfotransferase	209		1.00e-53
			AAH35282.1	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	209		1.00e-53
			BAC11177.1	unnamed protein product	209		2.00e-53
NM_033146	Mm.40667	F:(C-D)	Q9Y3B6	Protein CGI-112			
NP_149158.1		-2.03			393		1.00e-109
			NP_057133.1	CGI-112 protein	390		1.00e-108
			XP_033332.4	similar to Protein CGI-112	388		1.00e-108
NM_010324	Mm.19039	F:(C-D)	S29028	aspartate transaminase (EC 2.6.1.1) (clone 8C7)			
NP_034454.1		-2.01			810		0
			SI3035	aspartate transaminase (EC 2.6.1.1) - human	779		0
			NP_002070.1	aspartate aminotransferase 1; glutamic-oxaloacetic transaminase 1, soluble	779		0
			AAH00525.1	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	395		1.00e-109

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NM_016978	Mm.13694	F:(C-D)	NP_000265.1	ornithine aminotransferase precursor; Ornithine aminotransferase	781	0
NP_058674.1		-2.01	AAB35211.1	ornithine aminotransferase, OAT [human, gyrate atrophy of the choroid and retina (GACR) patient, Peptide Mutant, 439 aa]	780	0
			3319072	Chain A, Human Ornithine Aminotransferase Complexed With The Neurotoxin Gabaculine	727	0
			XP_093015.1	ar to Ornithine aminotransferase, mitochondrial precursor (Ornithine--oxo-acid aminotransferase)	393	e-109
NM_011172	Mm.28456	F:(C-D)	NP_057419.2	proline dehydrogenase (oxidase) 1; proline oxidase 2; p53 induced protein	889	0
NP_035302.1		-2	AAF21464.1	proline oxidase 2	888	0
			AAD24775.1	proline dehydrogenase; PRODH	822	0
			NP_005965.1	proline dehydrogenase; proline oxidase 2	821	0
			BAB33323.1	KIAA1653 protein	239	9.00e-63
			NP_067055.1	kidney and liver proline oxidase 1	200	6.00e-51
NM_013809	Mm.10231	F:(C-D)	NP_000757.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	563	1.00e-159
NP_038837.1	2	-2	Q16696	Cytochrome P450 2A13 (CYP1A13)	558	1.00e-158
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 -	555	1.00e-158
			NP_000753.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	553	1.00e-157
			P11509	Cytochrome P450 2A6 (CYP1A6) (Coumarin 7-hydroxylase) (IIA3) (CYP2A3) (P450(I))	552	1.00e-157
			AAF13600.1	cytochrome P450-2A6	551	1.00e-157
			1609083A	cytochrome P450IIA	551	1.00e-156
			CAA32097.1	cytochrome P-450IIA (AA 1 - 489)	551	1.00e-156
			P20853	Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)	543	1.00e-154
			C34271	cytochrome P450 2A4 - human	543	1.00e-154
			NP_000755.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 1	540	1.00e-153

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	I38965	cytochrome P450 - human	540	1.00e-153
	I38967	cytochrome P450 - human	529	1.00e-150
	CAA32117.1	P-450 IIA3 protein (1 is 3rd base in codon)	518	1.00e-146
	NP_000765.2	cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; similar to xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to		
		cytochrome P450, subfamily IIF, polypeptide 1 (H. sapiens)	516	1.00e-146
	NP_000758.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	516	1.00e-146
	NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		
	AAB23864.2	cytochrome P-450	514	1.00e-145
	BAA00123.1	cytochrome P-450	514	1.00e-145
	PI1713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	514	1.00e-145
	AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	512	1.00e-145
	NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	512	1.00e-145
	PI0632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	511	1.00e-144
	AAH20596.1	Unknown (protein for MGC:22146)	511	1.00e-144
	AAL69652.1	cytochrome P450 2F1	509	1.00e-144
	AAF13602.1	cytochrome P450-2B6	509	1.00e-144
	1506290A	cytochrome P450	509	1.00e-144
	NP_000761.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1		
	AAA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	508	1.00e-144
	S66382	cytochrome P450 2C8 - human	507	1.00e-143
			506	1.00e-143

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		AAB35292.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	506	1.00e-143
		F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19 - human	506	1.00e-143
		NP_000763.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18;		
			cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17;		
			microsomal monooxygenase; flavoprotein-linked monooxygenase	502	1.00e-142
		AA52161.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	502	1.00e-142
		P33260	ome P450 2C18 (CYP11C18) (P450-6B/29C)	500	1.00e-141
		P24903	Cytochrome P450 2F1 (CYP11F1)	496	1.00e-140
		I52418	cytochrome P450 - human	475	1.00e-133
		I38966	cytochrome P450 - human	467	1.00e-131
		NP_000764.1	cytochrome P450, subfamily IIE, polypeptide 1; microsomal monooxygenase;		
			xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450,		
			subfamily IIE (ethanol-inducible)	464	1.00e-130
		AAF13601.1	cytochrome P450-2E1	464	1.00e-130
		AAD13753.1	cytochrome P450 2E1	460	1.00e-129
		NP_085125.1	cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member		
			predicted from ESTs; cytochrome P540, subfamily IIS, polypeptide 1	455	1.00e-127
		BAB55227.1	unnamed protein product	451	1.00e-126
		NP_085079.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 2	445	1.00e-125
		AA52159.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	418	1.00e-116
		NP_110518.1	cytochrome P450, subfamily IIC, polypeptide 8 isoform 2; mephenytoin		
			4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase;		
			flavoprotein-linked monooxygenase; P450 form 1	406	1.00e-113
		G38462	cytochrome P450 2C17 - human (fragment)	404	1.00e-112
		AA52143.1	cytochrome P450-IIIB	389	1.00e-108
		S21423	cytochrome P450 2C - human	382	1.00e-106
		NP_000766.2	cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2;		
			microsomal monooxygenase; flavoprotein-linked monooxygenase; Cytochrome		
			P450, subfamily IIJ (arachidonic acid epoxidase),	367	1.00e-101

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				BAB85489.1	cytochrome P450 2J2	367	1.00e-101
				O4HUPB	cytochrome P450 2A3, hepatic - human	329	9.00e-90
				AAA53500.1	cytochrome P450 IID6	313	7.00e-85
				NP_000097.1	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		
5	NM_008184	Mm.31041	F:(C-D)	AAA59203.1	glutathione transferase M1	311	2.00e-84
	NP_032210.1		-1.78	XP_002155.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)	342	3.00e-9
				pdb 1GTU	Glutathione S-Transferase; Chain: A, B, C, D; Ec: 2.5.1.18	341	4.00e-9
				NP_000839.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	339	1.00e-9
				pdb 2GTU	Glutathione S-Transferase; Chain: A, B; Ec: 2.5.1.18	334	6.00e-9
				pdb 1HNA	Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C. 2.5.1.18) Mutant With Trp 214	332	2.00e-9
				NP_000841.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	328	3.00e-8
				P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	326	1.00e-8
				AAA57346.1	glutathione transferase M4	325	2.00e-8
				S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2) - human	325	3.00e-8
						325	3.00e-8

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			pdh4GTU]	Glutathione S-Transferase; Chain: A, B, C, D, E, F, G, H; Ec: 2.5.1.18	325	4.00e-8
			NP_000842.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	324	5.00e-8
			CAA48636.1	glutathione S-transferase	296	1.00e-7
			AAH17836.1	Similar to glutathione S-transferase M2 (muscle)	289	2.00e-7
			pdh3GTU]	Glutathione S-Transferase; Chain: A, B, C, D; Ec: 2.5.1.18	288	3.00e-7
			XP_042722.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	288	3.00e-7
			AAH08790.1	Unknown (protein for MGC:3704)	288	3.00e-7
			A35295	glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human	285	2.00e-7
			NP_671489.1	glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	283	2.00e-7
			XP_167023.1	similar to glutathione transferase M2 [Macaca fuscata]	257	7.00e-6
			NP_666533.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu 1	256	1.00e-6
AK003797 BAB23001.1	Mm.28252 F:(C-D) -1.71		CAD39140.1	hypothetical protein	319	2.00e-86

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				NP_057364.1	carboxylesterase-related protein	434	1.00e-120
AK014166	Mm.23082	F ₂ (C-D)		O76062	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase)		
BAB29187.1		-1.58			(Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1)		
					(Putative sterol reductase SR-1)	536	1.00e-169
				AAH12857.1	Similar to transmembrane 7 superfamily member 2	535	1.00e-169
				AAH09052.1	Similar to transmembrane 7 superfamily member 2	535	1.00e-169
				AAH38353.1	Similar to RIKEN cDNA 3110041O18 gene	469	1.00e-149
				NP_003264.1	transmembrane 7 superfamily member 2	514	1.00e-144
				XP_001795.5	similar to Lamin B receptor (Integral nuclear envelope inner membrane protein) (LMN2R)	411	1.00e-116
				AAA59495.1	Integral nuclear envelope inner membrane protein	411	1.00e-116
				NP_002287.1	Lamin B receptor	407	1.00e-115

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Master Table 1: Subtable 1B: Unfavorable Genes/Proteins

Main	Unigene	Behavior	Human Protein	Human Protein Name	Score	E-Value
NM_033373			BAA92054.1	unnamed protein product	598	1.0e-171
NP_203537.1	Mm.20127	U:(C-D)+ 7.74				
			NP_056330.3	keratin 23 isoform a; histone deacetylase inducible keratin 23; hyperacetylation-inducible type I keratin; keratin, type I cytoskeletal 23; cytokeratin 23; type I intermediate filament cytokeratin	597	1.0e-170
			AAH28356.1	type I intermediate filament cytokeratin	593	1.0e-169
			Q9C075	Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23).	591	1.0e-169
			TI7294	hypothetical protein DKFZp434G032.1	322	7.0e-88
			NP_775320.1	keratin 23 isoform b; histone deacetylase inducible keratin 23; hyperacetylation-inducible type I keratin; keratin, type I cytoskeletal 23; cytokeratin 23; type I intermediate filament cytokeratin	321	2.0e-87
			S37780	keratin 20, type I-like, cytoskeletal	299	6.0e-81
			NP_061883.1	keratin 20; cytokeratin 20; keratin, type I cytoskeletal 20	299	8.0e-81
			P08727	Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19).	287	3.0e-77
			NP_002267.2	keratin 19; keratin, type I cytoskeletal 19; keratin, type I, 40-kd; cytokeratin 19; 40-kDa keratin intermediate filament precursor gene	287	3.0e-77
			BAC04534.1	unnamed protein product	287	3.0e-77
			NP_000413.1	keratin 17	287	3.0e-77
			KRHU9	keratin 19, type I, cytoskeletal	286	7.0e-77
			NP_000214.1	keratin 12 (Meesmann corneal dystrophy); Keratin-12; keratin 12	283	3.0e-76
			NP_002266.2	keratin 15; keratin-15, basic; keratin-15, beta; type I cytoskeletal 15; cytokeratin 15	283	3.0e-76
			P19012	Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15).	283	3.0e-76
			NP_002265.1	keratin 13 isoform b; keratin, type I cytoskeletal 13; cytokeratin 13	281	2.0e-75
			NP_705694.1	keratin 13 isoform a; keratin, type I cytoskeletal 13; cytokeratin 13	281	2.0e-75

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			KRHU3	keratin 13, type I, cytoskeletal, long splice form	281	2.0e-75
			AAA59460.1	keratin type 16	278	1.0e-74
			NP_005548.2	keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16	278	2.0e-74
			JC4313	keratin 16, type I, cytoskeletal	278	2.0e-74
5			KRHUE	keratin 14, type I, cytoskeletal	277	2.0e-74
			AAH02690.1	Keratin 14	277	2.0e-74
			NP_000517.2	keratin 14; cytokeratin 14	277	2.0e-74
			NP_003762.1	type I hair keratin 6	264	3.0e-70
			AAH43581.1	Similar to keratin, hair, acidic, 6	264	3.0e-70
10			CAA51914.1	cytokeratin 20	263	4.0e-70
			NP_002271.2	type I hair keratin 5; Ha-5; hard keratin, type I, 5	257	3.0e-68
			NP_061889.1	keratin 24	256	6.0e-68
			CAA76387.1	type I hair keratin 5	256	8.0e-68
			Q92764	Keratin, type I cuticular HA5 (Hair keratin, type I HA5).	256	8.0e-68
15			CAA62286.1	HHa5 hair keratin type I intermediate filament	256	8.0e-68
			XP_039921.3	similar to keratin 17	253	5.0e-67
			AAH34697.1	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	252	8.0e-67
			P13645	Keratin, type I cytoskeletal...	252	8.0e-67
			NP_004129.2	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).	251	2.0e-66
20			O76009	type I hair keratin 3A; Ha-3I; hard keratin, type I, 3I; keratin, hair, acidic, 3A	251	2.0e-66
			KRHU0	keratin 10, type I, cytoskeletal	250	3.0e-66
			NP_002268.2	type I hair keratin 1; Ha-1; hard keratin, type I, 1; keratin, hair, acidic, 1	249	5.0e-66
			Q15323	Keratin, type I cuticular HA1 (Hair keratin, type I HA1).	249	7.0e-66
			O76011	Keratin, type I cuticular HA4 (Hair keratin, type I HA4).	248	1.0e-65
25			NP_002270.1	type I hair keratin 3B; Ha-3II; hard keratin, type I, 3II; keratin, hair, acidic, 3B	248	2.0e-65
			S60034	keratin Ha1, type I, hair - human	247	4.0e-65
			CAA57956.1	hair keratin acidic 3-II	246	5.0e-65
			AAH41070.1	similar to keratin, hair, acidic, 4	246	6.0e-65
			NP_066293.2	type I hair keratin 4; hard keratin, type I, 4	245	1.0e-64
30			NP_002269.2	type I hair keratin 2; Ha-2; hard keratin, type I, 2; keratin, hair, acidic, 2	245	1.0e-64

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			AAH12079.1	Similar to molybdenum cofactor sulfurase	319	2.00e-86
			NP_060417.1	molybdenum cofactor sulfurase	316	2.00e-85
S80191			AAH12418.1	Unknown (protein for MGC:9220)	828	0
AAB21335.1	F:(C-D) -1.61		NP_001257.3	carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver	824	0
			A48809	carboxylesterase; carboxylesterase 2 (liver)		
			BAA04650.1	carboxylesterase - human	823	0
			AAC60631.2	carboxylesterase	823	0
			I61085	acyl coenzyme A:cholesterol acyltransferase	822	0
			BAB85656.1	carboxylesterase - human	822	0
			AAD53175.1	brain carboxylesterase hBr2	822	0
			P23141	egaseyn	821	0
				Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)	821	0
			NP_036254.1	carboxylesterase 3; brain carboxylesterase BR3	794	0
			I57004	carboxylesterase - human (fragment).	734	0
			CAA37147.1	serine esterase N-terminal truncated (503 AA)	731	0
			AAA83932.1	carboxylesterase	631	1.00e-1
			BAA84995.1	brain carboxylesterase hBr1	594	79
			NP_003860.1	carboxylesterase 2; intestinal carboxylesterase; liver carboxylesterase-2	463	1.00e-1
			AAH32095.1	Similar to carboxylesterase 2 (intestine, liver)	463	29
			AAB03611.1	carboxylesterase hCE-2	462	1.00e-1
			CAD28531.1	hypothetical protein	449	29
						25

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			XP_091665.3	similar to keratin complex-1, acidic, gene C29; keratin complex-1, gene C29	244	2.0e-64
			Q14532	Keratin, type I cuticular HA2 (Hair keratin, type I HA2).	244	2.0e-64
			CAA57179.1	hair type I acidic keratin	244	2.0e-64
			NP_000215.1	keratin 18	243	4.0e-64
			CAA82315.1	cytokeratin 9	243	7.0e-64
			CAA31377.1	cytokeratin 18 (424 AA)	243	7.0e-64
			NP_000217.1	keratin 9	243	7.0e-64
			I37459	keratin Ha3-II, type I, hair	242	9.0e-64
			AAH00698.1	Keratin 18	242	1.0e-63
			AAA59468.1	keratin-10	239	6.0e-63
			CAA76389.3	type I hair keratin 7	236	5.0e-62
			NP_000412.1	keratin 10; Keratin-10	236	5.0e-62
			O76015	Keratin, type I cuticular HA8 (Hair keratin, type I HA8).	236	6.0e-62
			NP_006762.3	type I hair keratin 8	236	6.0e-62
			AAH09754.1	Similar to keratin 18	233	4.0e-61
			NP_003761.2	type I hair keratin 7	232	9.0e-61
			BAC03847.1	unnamed protein product	216	9.0e-56
NM_010721	Mm.4846	U:(C-D)+	NP_005564.1	lamin B1	878	0
NP_034851.1		7.08			878	0
			AAH12295.1	Similar to lamin B1	530	1.0e-149
			Q03252	Lamin B2	522	1.0e-146
			NP_005563.1	lamin A/C isoform 2; 70 kDa lamin	522	1.0e-146
			P02545	Lamin A/C (70 kDa lamin)	522	1.0e-146
			CAA27173.1	put. lamin A precursor (aa 1-702)	522	1.0e-146
			AAH33088.1	Similar to lamin A/C	414	1.0e-114
			A45023	lamin B2 - human (fragment)	403	1.0e-111
			AAA36160.1	lamin A protein	385	1.0e-105
NM_026228	Mm.30239	U:(C-D)+	NP_071437.1	up-regulated by BCG-CWS		
NP_080504.1		4.88			788	0

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				BAB55268.1	unnamed protein product	718	0
				BAA06685.1	KIAA0062	413	1.0e-114
				XP_046677.3	similar to KIAA0062	413	1.0e-114
				AAH15770.1	Unknown (protein for MGC:23235)	374	1.0e-102
				BAA96442.1	up-regulated by BCG-CWS	244	4.0e-63
NM_007702	Mm.449	U:(C-D)+		AAC34987.1	cell death activator CIDB-A		
NP_031728.1		4.7				340	3.0e-92
				AAH31896.1	Similar to cell death-inducing DFFA-like effector a	319	5.0e-86
AK013885	Mm.15337	U:(C-D)+		NP_006759	BRCA1 associated protein	914	0
NP_082503.1	2	4.18					
				AAC24200	BRCA1-associated protein 2	857	0
				AAB88538	putative DDB p127-associated protein	410	1.0e-114
NM_011995		U:(C-D)+		Q9Y6V0_2	[Segment 2 of 2] Piccolo protein (Aczonin).	4986	0
NP_036125.2	Mm.40996	4.17					
				T00332.	hypothetical protein KIAA0559 - human	1918	0
				XP_168530	similar to KIAA0559 protein	1882	0
				Q9Y6V0_1	[Segment 1 of 2] Piccolo protein (Aczonin).	578	1.0e-163
				T00062	hypothetical protein KIAA0434 - human (fragment).	537	1.0e-151
				NP_003449	bassoon; zinc finger protein 231; neuronal double zinc finger protein	537	1.0e-151
				CAA77176	Bassoon protein	537	1.0e-151
				T00634	hypothetical protein H_DJ0897G10.1	512	1.0e-144
				CAB60727	aczonin	419	1.0e-116
NM_013623		U:(C-D)+		NP_000598	orosomucoid 1 precursor; Orosomucoid-1 (alpha-1-acid glycoprotein-1); alpha-1-acid glycoprotein 1	165	4.0e-41
NP_038651.1	Mm.57239	4.05					
				AAH26238	orosomucoid 1	165	5.0e-41
				NP_000599	orosomucoid 2; alpha-1-acid glycoprotein, type 2	155	3.0e-38

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NM_008484				Q13751	Laminin beta-3 chain precursor (Laminin 5 beta 3) (Laminin B1k chain) (Kalinin B1 chain).	1806	0
NP_032510.1	Mm.4732	U(C-D)+ 4.05		A53612	laminin B1k chain precursor - human	1791	0
				NP_000219	laminin S B3 chain	1776	0
				.1			
				NP_002283	laminin, beta 2 precursor; laminin S	446	1.0e-124
				.2			
				P55268	Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain).	446	1.0e-124
				AAD43183.	laminin beta precursor; similar to AAB92586 (PID:g2708707)	434	1.0e-121
				1			
				A55677	laminin beta-2 chain precursor (version 1)	434	1.0e-121
				CAA56130.	beta2/S laminin chain	434	1.0e-121
				1			
				AAF22284.	laminin beta 1 related protein	428	1.0e-119
				1			
				NP_002282	laminin, beta 1 precursor	428	1.0e-119
				.1			
				AAH26018.	Similar to laminin, beta 1	317	8.0e-86
				1			
				AAM12527.	laminin alpha5 chain precursor	306	1.0e-82
				1			
				NP_005551	laminin alpha 5; laminin alpha-5 chain	306	1.0e-82
				.3			
				CAC22310.	bA157P1.1.1 (laminin alpha 5)	306	1.0e-82
				1			
				O15230	Laminin alpha-5 chain precursor	306	1.0e-82
				AAF75819.	Usher syndrome type IIa protein	280	1.0e-74
				1			

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			NP_009054	Usherin		280	1.0e-74
			.3				
			AAG53651.	netrin 4 precursor		280	1.0e-74
			1				
			AAC23748.	Usher syndrome type IIa protein		279	2.0e-74
			2				
			NP_067052	netrin 4; beta-netrin		278	4.0e-74
			.1				
			BAB67800.	KIAA1907 protein		275	4.0e-73
			1				
			AAH45172.	Similar to Laminin chain beta 2		264	6.0e-70
			1				
			NP_002284	laminin, gamma 1 precursor; formerly LAMB2		251	7.0e-66
			.2				
			P11047	Laminin gamma-1 chain precursor (Laminin B2 chain).		251	7.0e-66
			XP_113963	similar to laminin alpha 3b chain		250	9.0e-66
			.2				
			NP_006050	laminin, gamma 3 precursor		234	5.0e-61
			.2				
			Q9Y6N6	Laminin gamma-3 chain precursor (Laminin 12 gamma 3).		234	5.0e-61
			AAC51867.	laminin alpha 3b chain		230	1.0e-59
			1				
			BAC11679.	unnamed protein product		226	1.0e-58
			1				
			NP_004813	netrin 1; netrin 1, mouse, homolog of		213	1.0e-54
			.1				
			CAA41418.	laminin A chain		203	1.0e-51
			1				
			P25391	Laminin alpha-1 chain precursor (Laminin A chain).		202	3.0e-51

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				XP_209080 .1	similar to Laminin alpha-1 chain precursor (Laminin A chain)	202	3.0e-51
NM_026156	Mm.23739	U:(C-D)+ 3.75		XP_048364.2	similar to PP3898	1604	0
NP_080432.1				BAB15807.1	XAB2	1603	0
				BAA86491.1	KIAA1177 protein	1400	0
				NP_064581.1	HCNP protein; XPA-binding protein 2	1318	0
				AAH08778.1	Similar to HCNP protein; XPA-binding protein 2	1147	0
				BAB84861.1	FLJ00081 protein	607	1.0e-172
NM_013786				NP_003716	3-hydroxysteroid epimerase; oxidative 3-alpha-hydroxysteroid-dehydrogenase;	473	1.0e-133
		U:(C-D)+ 3.68			3(alpha->beta)-hydroxysteroid epimerase; retinol dehydrogenase; oxidoreductase; NAD+-dependent 3 alpha-hydroxysteroid dehydrogenase		
NP_038814.1	Mm.26719			AAB88252	oxidative 3 alpha hydroxysteroid dehydrogenase	442	1.0e-124
				AAC39922	sterol/retinol dehydrogenase	404	1.0e-112
				NP_003699	microsomal NAD+-dependent retinol dehydrogenase 4	399	1.0e-111
				NP_683695	orphan short-chain dehydrogenase / reductase; retinol dehydrogenase similar protein	312	6.0e-85
				NP_005762	NADP-dependent retinol dehydrogenase/reductase; 3-alpha hydroxysteroid dehydrogenase	300	3.0e-81
				Q92781	11-cis retinol dehydrogenase (11-cis RDH).	283	4.0e-76
				AAH28298	Similar to retinol dehydrogenase 5 (11-cis and 9-cis)	281	1.0e-75
				NP_002896	retinol dehydrogenase 5 (11-cis and 9-cis); retinol dehydrogenase 5 (11-cis and 9-cis)	272	1.0e-72
				AAD32458	retinol dehydrogenase homolog	267	2.0e-71
				AAF82748	retinol dehydrogenase homolog isoform-1	252	1.0e-66
NM_009345				P04053	DNA nucleotidylexotransferase (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase).	771	0
		U:(C-D)+ 3.66					
NP_033371.1	Mm.25620			AAA53100	terminal DON'T	767	0
				WXHU	DNA nucleotidylexotransferase (EC 2.7.7.31)	765	0
				AAA61136	terminal deoxynucleotidyltransferase	369	1.0e-101

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				NP_037416	polymerase (DNA directed), mu; polymerase (DNA-directed), mu; pol iota	333	7.0e-91
NM_013703				NP_003374	very low density lipoprotein receptor	1670	0
			U:(C-D)+ 3.61				
NP_038731.1	Mm4141			AAA61344. 1	very low density lipoprotein receptor	1668	0
				AAA53684. 1	very low density lipoprotein receptor	1665	0
				BAA03946. 1	very low density lipoprotein receptor	1610	0
				BAC03874. 1	unnamed protein product	1407	0
				NP_000518 .1	low density lipoprotein receptor precursor; LDL receptor; LDLR precursor	830	0
				AAF24515. 1	low density lipoprotein receptor	827	0
				NP_004622 .1	apolipoprotein E receptor 2 isoform 1 precursor; apolipoprotein E receptor 2	784	0
				1N7DA	Chain A, Extracellular Domain Of The Ldl Receptor	768	0
				NP_059992 .2	apolipoprotein E receptor 2 isoform 3 precursor; apolipoprotein E receptor 2	661	0
				NP_150643 .1	apolipoprotein E receptor 2 isoform 2 precursor; apolipoprotein E receptor 2	651	0
				CAA99509. 1	apolipoprotein E receptor 2 906	648	0
				NP_002323 .1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	464	1.0e-130
				NP_004516 .1	low density lipoprotein-related protein 2; megalin	459	1.0e-129

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				AAB02882. 1	glycoprotein 330	453	1.0e-127
				NP_061027 .1	low density lipoprotein-related protein 1B (deleted in tumors); low density lipoprotein receptor related protein-deleted in tumor	445	1.0e-124
				AAL38109. 1	candidate tumor suppressor protein	401	1.0e-111
				BAB70786. 1	unnamed protein product	387	1.0e-107
				AAL38108. 1	candidate tumor suppressor protein	366	1.0e-100
				1IJQA	Chain A, Crystal Structure Of The Ldl Receptor Ywtd-Egf Domain Pair.	352	2.0e-96
				BAA32468. 1	MEGF7	326	1.0e-88
				I38467	low density lipoprotein-related protein 2 - human	307	5.0e-83
				XP_035037 .2	similar to MEGF7	301	3.0e-81
				CAA38905. 1	alpha-2 macroglobulin receptor	270	9.0e-72
				AAC72791. 1	LDL receptor member LR3	245	3.0e-64
				JE0372	low density lipoprotein receptor related protein - human	245	3.0e-64
				NP_002326 .1	low density lipoprotein receptor-related protein 5; low density lipoprotein receptor-related protein 7; osteoporosis pseudoglioma syndrome	245	3.0e-64
				AAK52433. 1	low density lipoprotein receptor-related protein 5	245	3.0e-64
				NP_002327 .1	low density lipoprotein receptor-related protein 6; low density lipoprotein-related protein 6	245	3.0e-64

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				NP_001954	epidermal growth factor (beta-urogastrone); urogastrone	213	1.0e-54
				.1			
				AAL38107.1	candidate tumor suppressor protein	212	3.0e-54
NM_022414				NP_067080	neuroglobin	285	2.0e-76
NP_071859.1							
U70139				NP_036250.1	CCR4 carbon catabolite repression 4-like (S. cerevisiae); CCR4-like (carbon catabolite repression 4, S. cerevisiae)	603	1.0e-170
AAB62717.1							
				AAG01389.1	nocturnin	554	1.0e-155
				AAM81188.1	pol protein	375	1.0e-150
				AAK11553.1	polymerase	330	1.0e-132
				AAD51797.1	Gag-Pro-Pol protein	330	1.0e-132
				AAD21097.1	polymerase	330	1.0e-132
				AAA88033.1	pol/env ORF (bases 3878-8257) first start codon at 4172; Xxx; putative	327	1.0e-131
				AAK11554.1	polymerase	327	1.0e-131
				P10266	Endogenous retrovirus HERV-K10 putative pol polyprotein [Includes: Reverse transcriptase ; Endonuclease]	327	1.0e-131
				AAD51793.1	Gag-Pro-Pol-Env protein	327	1.0e-130
				AAD51796.1	Gag-Pro-Pol protein	312	1.0e-126
				AAL60056.1	pol protein	312	1.0e-126
				AAG01388.1	nocturnin	414	1.0e-113
				AAG18012.1	gag-pro-pol precursor protein	252	1.0e-113
				AAC63294.1	polymerase	167	3.1e-69
				AAC63291.1	polymerase	166	8.1e-68
				AAC63292.1	polymerase	166	1.1e-67

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				AAC63293.1	polymerase		163	2.1e-67
				AAC63290.1	polymerase		164	3.1e-67
NM_008137	Mm.22322	U:(C-D)+ 3.01		NP_004288.1	guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14		686	0
NP_032163.1				AAC50363.1	GTP-binding protein alpha q subunit		595	1.0e-169
				AAB64301.1	GTP-binding protein alpha q		593	1.0e-168
				P29992	Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)		591	1.0e-168
				P50148	Guanine nucleotide-binding protein G(q), alpha subunit		589	1.0e-167
				S71963	GTP-binding protein alpha-q - human (fragment)		589	1.0e-167
				NP_002058.1	guanine nucleotide binding protein (G protein), alpha 11 (Gq class); Guanine nucleotide-binding protein, Gq class, GNA11		589	1.0e-167
				AAB64303.1	guanine nucleotide binding protein alpha 11 subunit		588	1.0e-167
				NP_002063.1	guanine nucleotide binding protein (G protein), q polypeptide; Guanine nucleotide-binding protein (G protein), q; similar to guanine nucleotide binding protein (G protein), q polypeptide (H. sapiens)		588	1.0e-167
				NP_002059.1	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)		391	1.0e-107
				XP_009220.2	similar to GNA15; ALPHA-16		387	1.0e-106
				XP_095102.1	similar to Guanine nucleotide-binding protein, alpha-11 subunit (GL2)		369	1.0e-101
				P29777	Guanine nucleotide-binding protein G(O), alpha subunit 2		353	3.0e-96
				AAM12609.1	guanine nucleotide binding protein alpha oB		352	6.0e-96
				P04898	Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein)		346	6.0e-94
				CAB43212.2	hypothetical protein		345	7.0e-94
				AAA52556.1	guanine nucleotide-binding regulatory protein alpha-inhibitory subunit		345	7.0e-94
				NP_002061.1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2; Guanine nucleotide-binding protein (G protein), alpha-		345	7.0e-94
				NP_066268.1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O		342	8.0e-93
				AAH14627.1	Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2		342	8.0e-93
				AAA52581.1	guanine nucleotide-binding protein alpha-i subunit		341	1.0e-92

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			NP_002060.3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	341	2.0e-92
			NP_006487.1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3; 87U6	340	3.0e-92
			AAA52584.1	guanine nucleotide-binding protein	338	1.0e-91
			XP_170405.1	similar to Guanine nucleotide-binding protein G(T), alpha-3 subunit (Gustducin alpha-3 chain)	329	7.0e-89
5	AK009292 BAB26196.1	Mm.30487 U:(C-D)+ 2.94, U:(H1-D) 2.87	NP_005085.1	solute carrier family 27 (fatty acid transporter), member 4; fatty acid transport protein 4		
			AAH04268.1	Unknown (protein for IMAGE:3613739)	561	1.0e-158
			AAH09959.1	Unknown (protein for MGC:16752)	492	1.0e-138
			BAB55156.1	unnamed protein product	299	7.0e-80
			NP_077306.1	solute carrier family 27 member 3; fatty acid transport protein 3	295	1.0e-78
			NP_054750.1	very long-chain acyl-CoA synthetase homolog 1	295	1.0e-78
			NP_036386.1	solute carrier family 27 (fatty acid transporter), member 5; very long-chain acyl-CoA synthetase homolog 2; very long-chain acyl-CoA synthetase-related protein; likely ortholog of mouse solute carrier family 27 (fatty acid transporter), member 5	286	6.0e-76
			NP_003636.1	solute carrier family 27 (fatty acid transporter), member 2; very long-chain fatty-acid-coenzyme A ligase 1; very-long-chain acyl-CoA synthetase	276	6.0e-73
			AAH03654.1	Similar to hypothetical protein MGC4365	274	3.0e-72
15	M12573 AAA37863.1	Mm.6388 U:(C-D)+ 2.94	NP_005336.2	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1	249	8.0e-65
			P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	347	2.0e-94
			NP_005337.1	heat shock 70kDa protein 1B; heat shock 70kD protein 1B	347	2.0e-94
			A29160	dnaK-type molecular chaperone HSPA1L	345	6.0e-94
			XP_175177.1	heat shock 70kD protein 1-like	341	2.0e-92
			NP_005518.1	heat shock 70kDa protein 1-like; Heat-shock 70kD protein-like-1	312	6.0e-84
			BAA32521.1	Heat shock protein 70 testis variant	311	1.0e-83
			XP_166348.1	similar to heat shock protein	310	3.0e-83

				AAH34483.1	heat shock 70kD protein 1-like	308	1.0e-82
				AAH07276.1	Similar to heat shock cognate 71-kd protein	301	1.0e-80
				AAH15699.1	Unknown (protein for IMAGE:3906958)	301	1.0e-80
				NP_006588.1	Heat shock protein 70 testis variant	301	1.0e-80
5				AAH08907.1	Similar to heat shock 70kD protein 8	301	1.0e-80
				NP_068814.2	heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2	300	1.0e-80
				AAH36107.1	Unknown (protein for MGC:33922)	300	1.0e-80
				AAD11466.1	heat shock protein	300	1.0e-80
				CAA36062.1	heat shock protein 70B' (AA 355-643)	285	1.0e-75
10				XP_084070.5	similar to HEAT SHOCK 70 KD PROTEIN 6 (HEAT SHOCK 70 KD PROTEIN B)	285	1.0e-75
				AAH35665.1	heat shock 70kDa protein 6 (HSP70B')	285	1.0e-75
				NP_002146.1	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B'); Heat-shock 70kD protein-6 (HSP70B')	285	1.0e-75
	AK017185 BAB30625.1	Mm.26935	U:(C-D)+ 2.9	Q15771	Ras-related protein Rab-30		
15	NM_011889 Q9Z0J6	Mm.3132 5	U:(C-D)+ 2.8	JC5697	placental transforming growth factor-beta homolog	284	2.0e-76
				AAH00529	PLAB protein	281	2.0e-75
				AAC24456	prostate differentiation factor	281	2.0e-75
				AAC39537	prepro placental TGF-beta	281	2.0e-75
20				Q99988	Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1).	281	2.0e-75
				NP_004855	prostate differentiation factor; PTGF-beta; NSAID (nonsteroidal anti-inflammatory drug)-activated protein 1	280	6.0e-75
25	NM_011313 NP_035443.1	Mm.10014 4	U:(C-D)+ 2.77	NP_055439	S100 calcium-binding protein A6; calyculin; prolactin receptor-associated protein	142	3.0e-34

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AK005519 I49390	Mm.27289	U:(C-D)+ 2.7	Q14508	Major epididymis-specific protein E4 precursor (HE4) (Epididymal secretory protein E4) (WAP four-disulfide core domain protein 2)	131	1.0e-30
NM_008745						
NP_032771.1	Mm.3993	U:(C-D)+ 2.68	I73631	brain-derived neurotrophic factor receptor precursor, short splice form	868	0
			NP_006171	neurotrophic tyrosine kinase, receptor, type 2	846	0
			AAI67967	neurotrophin receptor tyrosine kinase type 2 truncated isoform	846	0
			AAI67966	neurotrophin receptor tyrosine kinase type 2 truncated isoform	845	0
			Q16620	BDNF/NT-3 growth factors receptor precursor (TrkB tyrosine kinase) (GP145-TrkB) (Trk-B)	845	0
			AAH13693	Unknown (protein for MGC:17113)	273	1.0e-72
			I73633	gene trkC protein	273	1.0e-72
			NP_002521	neurotrophic tyrosine kinase, receptor, type 3	273	1.0e-72
			CAA12029	TRKC	273	1.0e-72
			Q16288	NT-3 growth factor receptor precursor (TrkC tyrosine kinase) (GP145-TrkC) (Trk-C)	273	1.0e-72
			NP_002520	neurotrophic tyrosine kinase, receptor, type 1; Oncogene TRK	237	6.0e-62
			P04629	High affinity nerve growth factor receptor precursor (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A)	236	8.0e-62
			TVHUTT	nerve growth factor receptor precursor, high affinity	229	1.0e-59
			I1WVBX	Chain X, Ligand Binding Domain Of Human Trkb Receptor	223	9.0e-58
			I1HCFX	Chain X, Crystal Structure Of Trkb-D5 Bound To Neurotrophin-45	216	2.0e-55
NM_008063						
NP_032089.1	Mm.30087	U:(C-D)+ 2.68	NP_001458	glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1; Glucose-6-phosphate transporter-1	736	0
			AAD19898	glucose-6-phosphate transporter	734	0
			CAA76898	glucose 6-phosphate translocase	723	0

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				AAFI6691	PRO0685		533	1.0e-151
NM_019696				NP_062555	metallocarboxypeptidase CPX-1 precursor		1210	0
			U:(C-D)+	.1				
NP_062670.1	Mm.22224	2.66		Q96SM3	Potential carboxypeptidase X precursor (Metallocarboxypeptidase CPX-1).		1207	0
				BAC11661.	unnamed protein product		816	0
				1				
				XP_058409	similar to Potential carboxypeptidase-like protein X2 precursor		781	0
				.2				
				Q8N436	Potential carboxypeptidase-like protein X2 precursor		780	0
				AAH36789.	Unknown (protein for IMAGE:5752707)		780	0
				1	unnamed protein product		688	0
				BAC11672.				
				1				
				AAH38588.	Similar to AE binding protein 1		647	0
				1				
				NP_001120	adipocyte enhancer binding protein 1 precursor; AE-binding protein 1; aortic carboxypeptidase-like protein		647	0
				.2				
				JC5256	adipocyte transcription factor, AEBP1		647	0
				AAH32692.	Similar to carboxypeptidase X (M14 family)		404	1.0e-112
				1				
				AAH06393.	Similar to carboxypeptidase Z		382	1.0e-106
				1				
				NP_001864	carboxypeptidase E precursor		381	1.0e-105
				.1				
				NP_003643	CPZ gene product		380	1.0e-105
				.1				
				S12461	carboxypeptidase E - human		380	1.0e-105

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				BAA86053. 1	carboxypeptidase E	379	1.0e-105
				NP_001299 .1	carboxypeptidase N, polypeptide 1, 50kD precursor	373	1.0e-103
				AAH45549. 1	similar to carboxypeptidase D	340	5.0e-93
				AAC51775. 2	carboxypeptidase D	338	2.0e-92
				NP_001295 .2	carboxypeptidase D precursor	338	2.0e-92
				O75976	Carboxypeptidase D precursor (gp180).	338	2.0e-92
				A32619	carboxypeptidase M (EC 3.4.17.12) precursor - human	250	5.0e-66
				NP_001865 .1	carboxypeptidase M precursor	250	5.0e-66
NM_053261							
				U:(C-D)+			
NP_444491.1	Mm.34079	2.63		NP_055029	inositol(myo)-1(or 4)-monophosphatase 2	525	1.0e-149
				AAF07824	brain myo-inositol monophosphatase A2b; IMPase A2b	479	1.0e-135
				2HHMA	Chain A, Human Inositol Monophosphatase (E.C.3.1.3.25) Dimer Complex With Gadolinium		
				NP_005527	And Sulfate	327	2.0e-89
					inositol(myo)-1(or 4)-monophosphatase 1	327	2.0e-89
NM_008218				AAK37554. 1	hemoglobin alpha-1 globin chain	255	3.0e-68
NP_032244.1	Mm.19611	U:(C-D)+ 2.6	0	NP_000508 .1	alpha 2 globin	254	6.0e-68
				AAF72612. 1	alpha-2-globin	253	1.0e-67

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				hemoglobin alpha-2	253	1.0e-67
				Chain A, Deoxy Rhl.2 (Recombinant Hemoglobin).	252	2.0e-67
				Chain A, Deoxy Rhl.1 (Recombinant Hemoglobin).	252	2.0e-67
				Chain A, Alpha-Ferrous-Carbonmonoxy, Beta-Cobaltous-Deoxy Hemoglobin (T State).	252	2.0e-67
				Chain A, Hemoglobin Thionville Alpha Chain Mutant With Val 1 Replaced By Glu And An Acetylated Met Bound To The Amino Terminus.	251	3.0e-67
				Chain A, Hemoglobin (Alpha V1m) Mutant.	251	5.0e-67
				Chain A, R-State Human Carbonmonoxyhemoglobin Alpha-A53s	251	5.0e-67
				Chain A, Artificial Mutant (Alpha Y42h) Of Deoxy Hemoglobin.	250	9.0e-67
				Chain A, Hemoglobin A (Deoxy) Mutant With Arg A 141 And Arg C 141 Deleted (Del R(A 141), R(C 141)) (Desarg (141alpha)).	250	9.0e-67
				Chain A, Deoxy Hemoglobin (A-Glyglygly-C:v1m,L29w; B,D:v1m).	249	1.0e-66
				Chain A, Deoxy Hemoglobin (A,C:v1m,V62l; B,D:v1m,V67l).	249	1.0e-66
				Chain A, R State Human Hemoglobin [alpha V96w], Carbonmonoxy.	249	2.0e-66
				Chain A, Deoxyhemoglobin T38w (Alpha Chains), V1g (Alpha And Beta Chains).	248	4.0e-66
				Chain A, Deoxy Hemoglobin (A-Gly-C:v1m,L29f,H58q; B,D:v1m,L106w).	247	6.0e-66
				Chain A, Deoxy Hemoglobin (A-Glyglygly-C:v1m,L29f,H58q	247	6.0e-66
				Chain A, Deoxy Hemoglobin (A-Gly-C:v1m,L29w,H58q; B,D:v1m).	246	1.0e-65
				Chain A, Cyanomet Hemoglobin (A-Gly-C:v1m,L29f,H58q	246	1.0e-65
				Chain A, Deoxygenated Structure Of A Distal Pocket Hemoglobin Mutant.	246	2.0e-65
				alpha globin	213	2.0e-55

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NM_01887			U:(C-D)+ 2.54			cytochrome P450, family 39, subfamily A, polypeptide 1; oxysterol 7alpha-hydroxylase;			
NP_061375.1	Mm.17991			NP_057677 AAH10358		cytochrome P450, subfamily XXXIX (oxysterol 7 alpha-hydroxylase), polypeptide 1 oxysterol 7alpha-hydroxylase	712 710	0 0	
NM_009148									
NP_033174.1	Mm.6925		U:(C-D)+ 2.45	Q96A65 BAB21790		Exocyst complex component Sec8 KIAA1699 protein	1748 1733	0 0	
				CAD39134 AAF66445		hypothetical protein REC8	1332 1147	0 0	
				BAB14225 AAH26174		unnamed protein product Similar to secretory protein SEC8	1046 842	0 0	
NM_013790				O15440		Multidrug resistance-associated protein 5 (Multi-specific organic anion transporter-C) (MOAT-C) (pABC11) (SMRP).	2487	0	
NP_038818.1	Mm.20845		U:(C-D)+ 2.45	NP_005679 .1 AAD37716. 1 BAA76608. 1 JC5667		ATP-binding cassette, sub-family C, member 5; canalicular multispecific organic anion transporter C ABC protein MRP5 multidrug resistance protein, short type	2487 2487 2482	0 0 0	
				NP_150229 .1 AAK58869. 1		ATP-binding cassette, sub-family C, member 12 isoform e; multidrug resistance-associated protein 9 ATP-binding cassette protein C11	1703 1098 981	0 0 0	

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			NP_149163 .2	ATP-binding cassette, sub-family C, member 11 isoform a; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11	980	0
			AAK19755. 1	ATP-binding cassette transporter MRP8	979	0
			AAL99902. 1	ATP-binding cassette protein C11 isoform A	910	0
			NP_660187 .1	ATP-binding cassette, sub-family C, member 11 isoform b; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11	910	0
			AAL79528. 1	ATP-binding cassette protein C12 isoform A	754	0
			NP_660188 .1	ATP-binding cassette, sub-family C, member 12 isoform a; multidrug resistance-associated protein 9	753	0
			AAL88745. 1	multidrug resistance-associated protein	643	0
			AAC27077. 1	ABC transporter MOAT-B isoform	642	0
			NP_005836 .1	ATP-binding cassette, sub-family C, member 4; canalicular multispecific organic anion transporter (ABC superfamily)	642	0
			NP_063957 .1	ATP-binding cassette, sub-family C, member 1 isoform 7; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	642	0
			AAB83979. 1	multidrug resistance protein	642	0
			NP_004987 .1	ATP-binding cassette, sub-family C, member 1 isoform 1; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	642	0

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			NP_063956 .1	ATP-binding cassette, sub-family C, member 1 isoform 6; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	642	0
			AAB09422. 1	canalicular multispecific organic anion transporter	640	0
			DVHUAR	multidrug resistance protein (cell line H69AR)	639	0
			NP_000383 .1	ATP-binding cassette, sub-family C (CFTR/MRP), member 2; canalicular multispecific organic anion transporter	635	0
			NP_064693 .1	ATP-binding cassette, sub-family C, member 9 isoform SUR2B; sulfonyleurea receptor 2A	634	0
			S71841	multidrug resistance protein, canalicular	633	0
			CAB45309. 1	multidrug resistance protein 2 (MRP2)	632	1.0e-180
			AAL79529. 1	ATP-binding cassette protein C12 isoform B	624	1.0e-178
			NP_660189 .1	ATP-binding cassette, sub-family C, member 12 isoform b; multidrug resistance-associated protein 9	624	1.0e-178
			AAN17334. 1	ATP-binding cassette protein C4 splice variant A	621	1.0e-177
			CAC36037. 1	bA464I2.1 (ATP-binding cassette, sub-family C (CFTR/MRP), member 4)	619	1.0e-176
			NP_005682 .1	ATP-binding cassette, sub-family C, member 9 isoform SUR2A; sulfonyleurea receptor 2A	617	1.0e-176
			AAD01430. 1	MRP3	610	1.0e-174
			NP_003777 .2	ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter	610	1.0e-174
			CAA76658. 2	multidrug resistance protein 3 (ABCC3)	610	1.0e-174

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			BAA28146. 1	multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2)	610	1.0e-174
			JE0336	canalicular multispecific organic anion transporter	609	1.0e-173
			AAO40749. 1	truncated ABCC12 protein	586	1.0e-166
			CAC69553. 1	multidrug resistance associated protein	583	1.0e-166
			BAA92227. 1	FLJ00002 protein	579	1.0e-164
			NP_258261 .2	ATP-binding cassette, sub-family C, member 10; multidrug resistance-associated protein 7	579	1.0e-164
			AAC36724. 1	sulfonylurea receptor 1	572	1.0e-162
			Q09428	Sulfonylurea receptor 1	572	1.0e-162
			AAB02278. 1	sulfonylurea receptor	571	1.0e-162
			AAB02418. 1	alternative splice (exon 17)	571	1.0e-162
			AAK39642. 1	multidrug resistance-associated protein 7	569	1.0e-161
			NP_000343 .1	ATP-binding cassette, sub-family C, member 8; Sulfonylurea receptor; sulfonylurea receptor (hyperinsulinemia)	567	1.0e-161
			NP_064694 .1	ATP-binding cassette, sub-family C, member 9 isoform SUR2A-delta-14; sulfonylurea receptor 2A	555	1.0e-157
			AAB83983. 1	multidrug resistance protein	536	1.0e-152
			NP_063955 .1	ATP-binding cassette, sub-family C, member 1 isoform 5; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	536	1.0e-152

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				AAB83981. 1	multidrug resistance protein	531	1.0e-150
				NP_063915 .1	ATP-binding cassette, sub-family C, member 1 isoform 2; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	531	1.0e-150
				AAB83980. 1	multidrug resistance protein	530	1.0e-150
				NP_063953 .1	ATP-binding cassette, sub-family C, member 1 isoform 3; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	530	1.0e-150
				NP_001162 .2	ATP-binding cassette, sub-family C, member 6; anthracycline resistance-associated	509	1.0e-143
				AAD51293. 1	multi-specific organic anion transporter-E	506	1.0e-142
				NP_063954 .1	ATP-binding cassette, sub-family C, member 1 isoform 4; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein	461	1.0e-129
				AAB83982. 1	multidrug resistance protein	461	1.0e-129
				T43469	hypothetical protein DKFZp434L0827.1	411	1.0e-114
				BAB15736. 1	FLJ00036 protein	410	1.0e-113
				AAB71756. 1	multidrug resistance-associated protein homolog	386	1.0e-106
				AAC15784. 1	Multiple drug resistance gene MRP1 (5' partial)	363	1.0e-99
				AAC05808. 1	Multiple drug resistance gene MRP1 (partial)	322	4.0e-87
				AAH07229. 1	Unknown (protein for IMAGE:2957862)	319	3.0e-86

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AAH01636. 1	Unknown (protein for IMAGE:3355848)	311	6.0e-84
NP_064421. .1	ATP-binding cassette, sub-family C, member 3 isoform MRP3A; canicular multispecific organic anion transporter	307	1.0e-82
AAA99227. 1	sulfonylurea receptor	300	1.0e-80
NP_000483 .2	cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7); cystic fibrosis transmembrane conductance regulator; ATP-binding cassette, sub-family C member 7; CFTR/MRP	296	2.0e-79
P13569	Cystic fibrosis transmembrane conductance regulator (CFTR) (cAMP-dependent chloride channel).	296	2.0e-79
AAD38185. 1	MRP3s1 protein	288	5.0e-77
AAH41560. 1	Similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 4	274	1.0e-72
CAA65019. 1	anthracycline resistance associated protein	264	1.0e-69
AAH24103. 1	Similar to hypothetical protein FLJ000002	242	3.0e-63
AAB46340. 1	cystic fibrosis transmembrane conductance regulator	237	1.0e-61
NP_061338 .1	ATP-binding cassette, subfamily B, member 4 isoform C; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	235	5.0e-61

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			NP_000434.1	ATP-binding cassette, subfamily B, member 4 isoform A; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	232	4.0e-60
			NP_000918.1	ATP-binding cassette, sub-family B (MDR/TAP), member 1; P glycoprotein 1/multiple drug resistance 1; P-glycoprotein-1/multiple drug resistance-1; multidrug resistance 1	232	5.0e-60
			AAA59575.1	P-glycoprotein	232	5.0e-60
			P08183	Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).	232	5.0e-60
			AAB46341.1	coded for by human cDNA M96936 (NID:g180293)	227	1.0e-58
			NP_061337.1	ATP-binding cassette, subfamily B, member 4 isoform B; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	226	3.0e-58
			AAH39085.1	Similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 11	215	6.0e-55
			T34527	hypothetical protein DKFZp434I2115.1	211	6.0e-54
			AAB46352.1	transmembrane chloride conductor protein	210	1.0e-53
AK018132	Mm.41370	U:(C-D)+ 2.44	AAH12375.1	Similar to KIAA1001 protein	903	0
BAB31086.1			NP_055775.1	KIAA1001 protein	901	0
			AAB03341.1	arylsulfatase A	266	8.0e-70
			NP_000478.2	arylsulfatase A precursor	266	8.0e-70
			AAH14210.1	Similar to arylsulfatase A	266	1.0e-69

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				pdj1E2S	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8;	262	2.0e-68
				pdj1E3C	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8;	261	3.0e-68
				pdj1E1Z	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8	261	3.0e-68
				pdj1AUK	Human Arylsulfatase A	261	4.0e-68
				pdj1E33	Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8	257	5.0e-67
				NP_000503.1	N-acetylgalactosamine-6-sulfatase precursor; Galactosamine (N-acetyl)-6-sulfate sulfatase; chondroitinase	251	3.0e-65
				AAH22389.1	Unknown (protein for MGC:24090)	237	5.0e-61
				NP_004033.1	arylsulfatase F	237	7.0e-61
				XP_035467.1	similar to arylsulfatase F	235	2.0e-60
				AAH20229.1	Unknown (protein for MGC:31932)	233	1.0e-59
				NP_001660.1	arylsulfatase D precursor, isoform a	230	7.0e-59
NM_008532					Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated antigen) (KSA) (KS 1/4 antigen) (Cell surface glycoprotein Trop-1).	446	1.0e-125
NP_032558.1	Mm.4259	U:(C-D)+ 2.41		P16422	tumor-associated calcium signal transducer 1 precursor; membrane component, chromosome 4, surface marker (35kD glycoprotein); MK-1 antigen; antigen identified by monoclonal antibody AUA1	446	1.0e-125
				NP_002345	AUA1	444	1.0e-124
				AAA35723	epithelial glycoprotein (EGP) precursor	265	2.0e-70
				A48149	carcinoma-associated antigen GA733-1 precursor		
					tumor-associated calcium signal transducer 2 precursor; membrane component, chromosome 1, surface marker 1 (40kD glycoprotein, identified by monoclonal antibody GA733); epithelial glycoprotein-1	263	5.0e-70
				NP_002344	Tumor-associated calcium signal transducer 2 precursor (Pancreatic carcinoma marker protein GA733-1) (Cell surface glycoprotein Trop-2).	262	1.0e-69
				P09758			
AK004984	Mm.15875	U:(C-D)+		AAAS3500.1	cytochrome P450 IID6	186	1.0e-45
BAB23719.1	1	2.38					

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				NP_000097.1	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	186	1.0e-45
				AAA35737.1	debrisoquine 4-hydroxylase	184	3.0e-45
				AAA36403.1	cytochrome P450db1	184	3.0e-45
NM_013722							
NP_038750.1	Mm.10364	U:(C-D)+		O14994	Synapsin III	712	0
		2.35		NP_003481	synapsin III isoform IIIa	710	0
				NP_598344.	synapsin III isoform IIIc	710	0
				NP_598343	synapsin III isoform IIIb	701	0
				JC4940.	synapsin IIb	531	1.0e-150
				NP_598328	synapsin II isoform IIa	530	1.0e-150
				NP_003169	synapsin II isoform IIb	530	1.0e-150
				Q92777	Synapsin II	529	1.0e-150
				AAC33789	synapsin IIb	529	1.0e-150
				NP_598006	synapsin I isoform Ib; brain protein 4.1	509	1.0e-144
				NP_008881	synapsin I isoform Ia; brain protein 4.1	509	1.0e-144
				A35363	synapsin I splice form a	509	1.0e-144
				P17600	Synapsin I (Brain protein 4.1).	508	1.0e-144
				AAC41931	synapsin Ib	508	1.0e-144
NM_008439							
NP_032465.1	Mm.22451	U:(C-D)+					
		2.35		NP_006479	ketohexokinase isoform b	541	1.0e-154
				NP_000212	ketohexokinase isoform a	496	1.0e-140
				AAH06233	ketohexokinase (fructokinase)	496	1.0e-140
				CAA55346	ketohexokinase	416	1.0e-116
				CAA06409	ketohexokinase	333	3.0e-91
				CAA70516	ketohexokinase	209	4.0e-54

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[illegible]

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				O95622	Adenylate cyclase, type V (ATP pyrophosphate-lyase) (Adenylyl cyclase).	1290	0
				NP_0011106.1	adenylate cyclase 8; Adenylyl cyclase-8, brain	713	0
				S48687	type VIII adenylyl cyclase - human	713	0
				NP_065433.1	adenylate cyclase 2; ATP pyrophosphate-lyase; type II adenylate cyclase; adenylyl cyclase 2; adenylate cyclase II; 3',5'-cyclic AMP synthetase	660	0
				Q08462	Adenylate cyclase, type II (ATP pyrophosphate-lyase) (Adenylyl cyclase).	624	1.0e-178
				NP_640340.2	adenylate cyclase 4; adenylate cyclase type IV	616	1.0e-176
				CAD62613.1	unnamed protein product	616	1.0e-176
				Q08828	Adenylate cyclase, type I (ATP pyrophosphate-lyase) (Ca(2+)/calmodulin activated adenylyl cyclase).	601	1.0e-171
				NP_0011105.1	adenylate cyclase 7	600	1.0e-171
				NP_004027.1	adenylate cyclase 3; adenylyl cyclase, type III; ATP pyrophosphate-lyase	591	1.0e-168
				BAA25437.1	KIAA0511 protein	584	1.0e-166
				AAF82479.1	adenylyl cyclase type VI	409	1.0e-113
				PQ0227	adenylate cyclase (EC 4.6.1.1), brain - human (fragment).	372	1.0e-102
				BAB71270.1	unnamed protein product	320	2.0e-86
				I37136	adenylate cyclase (EC 4.6.1.1)	312	4.0e-84
				AAC28647.1	adenylyl cyclase	306	3.0e-82

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			AAH39891. 1	Similar to adenylate cyclase 7	288	5.0e-77
			BAC11613. 1	unnamed protein product	269	4.0e-71
			BAA25446. 2	KIAA0520 protein	210	2.0e-53
			NP_001107 .1	adenylate cyclase 9	210	2.0e-53
			O60503	Adenylate cyclase, type IX (ATP pyrophosphate-lyase) (Adenylyl cyclase).	210	2.0e-53
			CAB65084. 1	adenylyl cyclase type IX	207	2.0e-52
AK007384	U:(C-D)+		NP_001047	sulfotransferase family, cytosolic, 1C, member 1 isoform a;	531	1.0e-151
BAB25002.1	Mm.19320 2.27		.1	sulfotransferase 1C1		
			AAF72802. 1	sulfotransferase 1C1	489	1.0e-138
			NP_006579 .2	sulfotransferase family, cytosolic, 1C, member 2; sulfotransferase family, cytosolic, 1C, member C2; sulfotransferase 1C2	384	1.0e-107
			O75897	Sulfotransferase 1C2 (SULT1C) (SULT1C#2).	384	1.0e-106
			AAB65154. 1	thyroid hormone sulfotransferase	358	5.0e-95
			AAH10895. 1	Unknown (protein for MGC:13356)	358	5.0e-95
			JC5885	thyroid hormone sulfotransferase (EC 2.8.2.-) B2 -	357	1.0e-98
			P50225	phenol-sulfating phenol sulfotransferase 1 (P-PST) (Thermostable phenol sulfotransferase) (Ts-PST) (HAST1/HAST2) (ST1A3).	343	2.0e-94

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		AAH00923. 1	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1, isoform a	343	3.0e-94
		I57945	phenol-sulfating phenol sulfotransferase	342	4.0e-94
		JC5248	aryl sulfotransferase (EC 2.8.2.1) HAST2	342	5.0e-94
		AAB31317. 1	aryl sulfotransferase ST1A3 [human, liver, Peptide, 295 aa].	342	5.0e-94
		JC2523	aryl sulfotransferase (EC 2.8.2.1) brain isoform	341	1.0e-93
		S52399	aryl sulfotransferase (EC 2.8.2.1)	339	3.0e-93
		NP_001045 .1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; thermostable phenol sulfotransferase; phenolic-metabolizing (P) form of PST; arylamine sulfotransferase; aryl sulfotransferase; phenol-preferring phenol sulfotransferase2; phenol-sulfating phenol sulfotransferase 2	337	1.0e-92
		NP_003157 .1	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; thermolabile phenol sulfotransferase; catecholamine-sulfating phenol sulfotransferase; aryl sulfotransferase; thermolabile (monoamine, M form) phenol sulfotransferase; monoamine-sulfating phenosulfotransferase; placental estrogen sulfotransferase; monoamine-preferring sulfotransferase	334	1.0e-91
		P50226	Phenol-sulfating phenol sulfotransferase 2 (P-PST) (ST1A2).	334	1.0e-91
		S52791	aryl sulfotransferase (EC 2.8.2.1)	333	2.0e-91
		AAC51149. 1	arylamine sulfotransferase	333	2.0e-91
		AAC99987. 1	aryl sulfotransferase	330	3.0e-90
		NP_005411 .1	sulfotransferase, estrogen-preferring; estrogen sulfotransferase	315	9.0e-86

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203

			AAH27956. 1	sulfotransferase, estrogen-preferring	313	2.0e-85
			1HY3A	Chain A, Crystal Structure Of Human Estrogen Sulfotransferase V269e Mutant In The Presence Of Paps	312	4.0e-85
			1J99A	Chain A, Crystal Structure Of Human Dehydroepiandrosterone Sulfotransferase In Complex With Substrate	212	6.0e-55
			AAA35758. 1	dehydroepiandrosterone sulfotransferase	211	1.0e-54
			AAH23169. 2	alcohol/hydroxysteroid sulfotransferase; hSta	211	1.0e-54
			Q06520	Alcohol sulfotransferase (Hydroxysteroid Sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase) (DHEA-ST) (ST2)	211	1.0e-54
			AAC78553. 1	hydroxysteroid sulfotransferase SULT2B1a	211	1.0e-54
			AAC78498. 1	hydroxysteroid sulfotransferase SULT2B1a	211	1.0e-54
			1EFHA	Chain A, Crystal Structure Of The Human Hydroxysteroid Sulfotransferase In The Presence Of Pap.	211	1.0e-54
			AAC78499. 1	hydroxysteroid sulfotransferase SULT2B1b	211	1.0e-54
NM_013738						
	Mm.10338	U:(C-D)+				
NP_038766.1	0	2.25	NP_057529	pleckstrin 2; pleckstrin 2 (mouse) homolog	657	0
			AAH08056	pleckstrin 2 (mouse) homolog	654	0
			NP_002655	pleckstrin; p47	238	1.0e-62
			AAH18549	Unknown (protein for MGC:17111)	238	2.0e-62
			1408254A	protein kinase C substrate protein P47	237	3.0e-62

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204

NM_013757			NP_542775	synaptotagmin-like 4 (granuphilin-a)	1140	0
NP_038785.1	Mm.38674	U:(C-D)+ 2.22	.1			
			BAC04287. 1	unnamed protein product	1136	0
			CAC16061. 1	bA524D16A.2.1 (novel protein similar to mouse granuphilin-a)	842	0
			CAC16062. 1	bA524D16A.2.2 (novel protein similar to mouse granuphilin-b)	477	1.0e-134
			NP_620135 .1	synaptotagmin-like 5	421	1.0e-117
			BAB15030. 1	unnamed protein product	286	2.0e-76
			NP_115755 .2	synaptotagmin-like 2 isoform b; chromosome 11 synaptotagmin	285	2.0e-76
			BAB13423. 1	KIAA1597 protein	279	2.0e-74
			NP_116561 .1	synaptotagmin-like 2 isoform a; chromosome 11 synaptotagmin	278	4.0e-74
			AAH09224. 1	Unknown (protein for IMAGE:3942111)	245	3.0e-64
			AAK67636. 1	hypothetical protein SB146	245	3.0e-64
			NP_116261 .1	NADPH oxidase-related, C2 domain-containing protein	245	4.0e-64
			AAH15764. 1	Similar to NADPH oxidase-related, C2 domain-containing protein	245	4.0e-64
			AAH35725. 1	Similar to NADPH oxidase-related, C2 domain-containing protein	245	4.0e-64

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205

				XP_087804.1	similar to synaptotagmin-like protein 3-a	213	2.0e-54
NM_009368							
5	NP_033394.1	Mm.1291	U:(C-D)+ 2.22	NP_003230	transforming growth factor, beta 3	766	0
				CAA33024	transforming growth factor-beta 3	762	0
				AAH18503	Similar to transforming growth factor, beta 3	542	1.0e-154
				NP_003229	transforming growth factor, beta 2	432	1.0e-120
				AAA50405	transforming growth factor beta 2	427	1.0e-119
10				B31249	transforming growth factor beta-2 precursor, long form	422	1.0e-117
				P01137	Transforming growth factor beta 1 precursor (TGF-beta 1).	302	1.0e-81
					transforming growth factor, beta 1 (Camurati-Engelmann disease); transforming growth factor, beta 1; diaphyseal dysplasia 1, progressive (Camurati-Engelmann disease)	301	4.0e-81
				NP_000651	Human Transforming Growth Factor Beta 3, Crystallized From Peg 4000	248	3.0e-65
				ITGK	Transforming Growth Factor Type Beta 2 (Tgf-B2).	210	7.0e-54
15				ITFG	Chain A, Solution Structure Of Tgf-B1, Nmr, Models 18-33 Of 33 Structures	197	8.0e-50
				IKLDA			
	AK013002		U:(C-D)+ 2.21	AAH00120.1	general transcription factor IIF, polypeptide 1 (74kD subunit)		
	BAB28588.1			NP_002087.1	general transcription factor IIF, polypeptide 1 (74kD subunit)	387	1.0e-106
20				CAA45404.1	RAP74	387	1.0e-106
				pdh 1F3U	Transcription Initiation Factor Iif, Subunit; Chain: A, C, E, G; Fragment: Residues 2-119; Synonym: Transcription Initiation Factor Rap30	386	1.0e-106
	NM_013750					315	7.0e-85
			U:(C-D)+ 2.21		pleckstrin homology-like domain, family A, member 3; pleckstrin homology-like domain, family A, member 2		
25	NP_038778.1	Mm.34346		NP_036528	unnamed protein product	246	5.0e-65
				BAC11454		242	8.0e-64

206

NM_008471			P08727	Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19).	539	1.0e-153
NP_032497.1	Mm.1012	U:(C-D)+ 2.21				
			NP_002267 .2	keratin 19; keratin, type I cytoskeletal 19; keratin, type I, 40-kd; cytokeratin 19; 40-kDa keratin intermediate filament precursor gene	539	1.0e-153
			KRHU9	keratin 19, type I, cytoskeletal	539	1.0e-153
			NP_000413 .1	keratin 17	453	1.0e-127
			BAC04534. 1	unnamed protein product	453	1.0e-127
			KRHUE	keratin 14, type I, cytoskeletal	443	1.0e-124
			AAH02690. 1	Keratin 14	443	1.0e-124
			NP_000517 .2	keratin 15; keratin-15, basic; keratin-15, beta; type I cytoskeletal 15; cytokeratin 15	443	1.0e-124
			NP_002266 .2	keratin 15; keratin-15, basic; keratin-15; beta; type I cytoskeletal 15; cytokeratin 15	442	1.0e-124
			P19012	Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15).	442	1.0e-124
			NP_005548 .2	keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16	436	1.0e-122
			JC4313	keratin 16, type I, cytoskeletal	436	1.0e-122
			NP_705694 .1	keratin 13 isoform a; keratin, type I cytoskeletal 13; cytokeratin13	433	1.0e-121
			KRHU3	keratin 13, type I, cytoskeletal, long splice form	433	1.0e-121
			NP_002265 .1	keratin 13 isoform b; keratin, type I cytoskeletal 13; cytokeratin 13	432	1.0e-121
			AAA59460. 1	keratin type 16	431	1.0e-121

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207

			XP_039921 .3	similar to keratin 17	409	1.0e-114
			PI3645	Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).	386	1.0e-107
			AAH34697. 1	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)	386	1.0e-107
			KRHU0	keratin 10, type I, cytoskeletal	384	1.0e-106
			NP_000214 .1	keratin 12 (Meesmann corneal dystrophy); Keratin 12	380	1.0e-105
5			NP_000412 .1	keratin 10; Keratin-10	374	1.0e-103
			AAH43581. 1	Similar to keratin, hair, acidic, 6	365	1.0e-101
			NP_003762 .1	type I hair keratin 6	365	1.0e-101
			AAA59468. 1	keratin-10	361	1.0e-99
10			NP_002271 .2	type I hair keratin 5; Ha-5; hard keratin, type I, 5	353	3.0e-97
			CAA76387. 1	type I hair keratin 5	352	9.0e-97
			Q92764	Keratin, type I cuticular HA5 (Hair keratin, type I HA5).	352	9.0e-97
			CAA62286. 1	HHa5 hair keratin type I intermediate filament	352	9.0e-97
			BAC03847. 1	unnamed protein product	351	1.0e-96
			NP_061889 .1	keratin 24	350	2.0e-96
15			XP_091665 .3	similar to keratin complex-1, acidic, gene C29; keratin complex-1, gene C29	343	4.0e-94

208

			NP_002268 .2	type I hair keratin 1; Ha-1; hard keratin, type I, 1; keratin, hair, acidic, 1	342	9.0e-94
			Q15323	Keratin, type I cuticular HA1 (Hair keratin, type I HA1).	341	1.0e-93
			NP_002270 .1	type I hair keratin 3B; Ha-3II; hard keratin, type I, 3II; keratin, hair, acidic, 3B	341	1.0e-93
			NP_002269 .2	type I hair keratin 2; Ha-2; hard keratin, type I, 2; keratin, hair, acidic, 2	340	2.0e-93
			NP_004129 .2	type I hair keratin 3A; Ha-3I; hard keratin, type I, 3I; keratin, hair, acidic, 3A	340	3.0e-93
			CAA57956. 1	hair keratin acidic 3-II	340	3.0e-93
			NP_061883 .1	keratin 20; cytokeratin 20; keratin, type I cytoskeletal 20	340	3.0e-93
			O76009	Keratin, type I cuticular HA3-I (Hair keratin, type I HA3-I).	340	3.0e-93
			S37780	keratin 20, type I-like, cytoskeletal - human	339	6.0e-93
			S60034	keratin Ha1, type I, hair	337	2.0e-92
			AAH41070. 1	similar to keratin, hair, acidic, 4	337	2.0e-92
			Q14532	Keratin, type I cuticular HA2 (Hair keratin, type I HA2).	337	2.0e-92
			CAA57179. 1	hair type I acidic keratin	337	2.0e-92
			NP_066293 .2	type I hair keratin 4; hard keratin, type I, 4	337	3.0e-92
			O76011	Keratin, type I cuticular HA4 (Hair keratin, type I HA4).	334	1.0e-91
			I37459	keratin Ha3-II, type I, hair	332	5.0e-91
			NP_000217 .1	keratin 9	325	9.0e-89
			CAA82315. 1	cytokeratin 9	325	9.0e-89

209

			BAA94607. 1	keratin 19	313	4.0e-85
			CAA29248. 1	gene product (clone 266) (266, AA)	307	2.0e-83
			NP_000215 .1	keratin 18	306	5.0e-83
			AAH09754. 1	Similar to keratin 18	306	5.0e-83
			CAA31377. 1	cytokeratin 18 (424 AA)	306	5.0e-83
			AAA59199. 1	keratin 10	304	2.0e-82
			AAH00698. 1	Keratin 18	304	2.0e-82
			CAA51914. 1	cytokeratin 20	303	4.0e-82
			O76015	Keratin, type I cuticular HA4 (Hair keratin, type I HA4).	301	1.0e-81
			NP_006762 .3	type I hair keratin 8	301	1.0e-81
			CAA76389. 3	type I hair keratin 7	299	7.0e-81
			NP_003761 .2	type I hair keratin 7	294	2.0e-79
			NP_056330 .3	keratin 23 isoform a; histone deacetylase inducible keratin 23; hyperacetylation-inducible type I keratin; keratin, type I cytoskeletal 23; cytokeratin 23; type I intermediate filament cytokeratin	276	6.0e-74
			AAH28356. 1	type I intermediate filament; cytokeratin	275	8.0e-74

210

				BAA92054. 1	unnamed protein product	274	2.0e-73
				Q9C075	Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23).	273	5.0e-73
				XP_209012 .1	similar to keratin 17	263	5.0e-70
				XP_061644 .5	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)	246	7.0e-65
				AAB30058. 2	keratin	244	1.0e-64
				BAA19418. 1	mutant keratin 9	240	4.0e-63
				XP_066374 .1	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)	205	1.0e-52
				AAH33252. 1	Unknown (protein for IMAGE:5444378)	197	3.0e-50
NM_010707							
NP_034837.1	Mm.21033 6	U:(C-D)+ 2.2		NP_006140	galectin 4; lectin galactoside-binding soluble 4	471	133
AK007293	Mm.15975 3	U:(C-D)+ 2.19, U:(HI-D) +2.62		BAB67772.1	KIAA1879 protein		
BAB24937.1							
				NP_000763 .1	cytochrome P450, family 2, subfamily C, polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; microsomal monooxygenase; flavoprotein-linked monooxygenase	189	8.0e-47
NM_010003						737	0
NP_034133.1	Mm.42101	U:(C-D)+ 2.18		P33260	Cytochrome P450 2C18 (CYP1C18) (P450-6B/29C).	737	0

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			NP_000760 .1	cytochrome P450, family 2, subfamily C, polypeptide 19; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	724	0
			AAB23864. 2	cytochrome P-450	719	0
			BAA00123. 1	cytochrome P-450	719	0
			NP_000762 .2	cytochrome P450, family 2, subfamily C, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	719	0
			PI0632	Cytochrome P450 2C8 (CYP1IC8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase).	717	0
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19	716	0
			AAH20596. 1	Unknown (protein for MGC:22146)	716	0
			AAA52157. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	715	0
			1506290A	cytochrome P450	715	0
			P11713	Cytochrome P450 2C10 (CYP1IC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP).	715	0

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			NP_000761 .2	cytochrome P450, family 2, subfamily C, polypeptide 8 isoform 1; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	714	0
			AAB35292. 1	cytochrome P450 arachidonic acid epoxygenase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	712	0
			AAA52160. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	712	0
			AAA52161. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase.	701	0
			I52418	cytochrome P450 - human	662	0
			AAA52159. 1	cytochrome P-450 S-mephenytoin 4-hydroxylase	584	1.0e-166
			G38462	cytochrome P450 2C17 - human	573	1.0e-163
			NP_110518 .1	cytochrome P450, family 2, subfamily C, polypeptide 8 isoform 2; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	567	1.0e-161
			NP_000764. .1	cytochrome P450, family 2, subfamily E, polypeptide 1; cytochrome P450, subfamily IIE (ethanol-inducible), polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)	551	1.0e-157
			AAF13601. 1	cytochrome P450-2E1	550	1.0e-156
			S21423	cytochrome P450 2C - human	548	1.0e-155
			AAD13753. 1	cytochrome P450 2E1	546	1.0e-155

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			NP_000765 .2	cytochrome P450, family 2, subfamily F, polypeptide 1; cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	487	1.0e-137
			AAI69652. 1	cytochrome P450 2F1	482	1.0e-136
			NP_000758 .1	cytochrome P450, family 2, subfamily B, polypeptide 6; cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6	474	1.0e-133
			P24903	Cytochrome P450 2F1 (CYP2F1).	470	1.0e-132
			AAF13602. 1	cytochrome P450-2B6	469	1.0e-132
			NP_000757 .2	cytochrome P450, family 2, subfamily A, polypeptide 13; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	463	1.0e-130
			Q16696	Cytochrome P450 2A13 (CYP2A13).	460	1.0e-129
			NP_000753 .2	cytochrome P450, family 2, subfamily A, polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	457	1.0e-128
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6	457	1.0e-128
			1609083A	cytochrome P450IIA	455	1.0e-128
			CAA32097. 1	cytochrome P-450IIA (AA 1 - 489)	455	1.0e-128
			P11509	Cytochrome P450 2A6 (CYP2A6) (Coumarin 7-hydroxylase) (IIA3) (CYP2A3) (P450(I)).	455	1.0e-128
			AAF13600. 1	cytochrome P450-2A6	454	1.0e-128

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			NP_000755 .2	cytochrome P450, family 2, subfamily A, polypeptide 7 isoform 1; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	453	1.0e-127
			P20853	Cytochrome P450 2A7 (CYP1A7) (P450-IIA4).	452	1.0e-127
			C34271	cytochrome P450 2A4 - human	451	1.0e-126
			I38967	cytochrome P450 - human	446	1.0e-125
			I38965	cytochrome P450 - human	446	1.0e-125
			CAA32117. 1	P-450 IIA3 protein (1 is 3rd base in codon)	423	1.0e-118
			NP_085125 .1	cytochrome P450, family 2, subfamily S, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide 1	409	1.0e-114
			AAD13466. 1	cytochrome P-450 2C	408	1.0e-113
			BAB55227. 1	unnamed protein product	405	1.0e-112
			I38966	cytochrome P450 - human	389	1.0e-108
			NP_085079 .2	cytochrome P450, family 2, subfamily A, polypeptide 7 isoform 2; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7	376	1.0e-104
			NP_000766 .2	cytochrome P450, family 2, subfamily J, polypeptide 2; cytochrome P450, subfamily IIJ (arachidonic acid epoxigenase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase	373	1.0e-103
			BAB85489. 1	cytochrome P450 2J2	373	1.0e-103
			AAA52143. 1	cytochrome P450-IIB	354	2.0e-97

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			AAA53500. 1	cytochrome P450 IID6	332	8.0e-91
			NP_000097 .1	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing)-like 1	332	1.0e-90
			AAL31348. 1	S-mephenytoin 4-hydroxylase	324	2.0e-88
			CAA35915. 1	cytochrome P-450 HPH (120 AA)	315	1.0e-85
			AAH25761. 1	Similar to hypothetical protein FLJ20359	310	3.0e-84
			AAA35737. 1	debrisoquine 4-hydroxylase	279	1.0e-74
			NP_060251 .1	hypothetical protein FLJ20359	272	1.0e-72
			AAA36403. 1	cytochrome P450db1	271	2.0e-72
			AAD30164. 1	cytochrome P450 epoxigenase	270	6.0e-72
			O4HUPB	cytochrome P450 2A3, hepatic - human	264	3.0e-70
			AAD13467. 1	cytochrome P-450 2C	256	5.0e-68
			XP_058459 .6	similar to cytochrome P450, family 2, subfamily r, polypeptide 1; cytochrome P450, 2r1	239	9.0e-63
			AAC50809. 1	cytochrome P450 CYP1B1	238	3.0e-62

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			NP_000095 .1	cytochrome P450, family 1, subfamily B, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile); microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	238	3.0e-62
			AAH20754. 1	Similar to cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9	229	9.0e-60
			AAL31347. 1	S-mephenytoin 4-hydroxylase	224	2.0e-58
			CAA26458. 1	cytochrome P(1)-450	221	2.0e-57
			NP_000490 .1	cytochrome P450, family 1, subfamily A, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	220	4.0e-57
			AAA52139. 1	cytochrome P-450-1	219	7.0e-57
NM_019875			NP_062571 U:(C-D)+ .1	ATP-binding cassette, sub-family B, member 9 isoform 1	1397	0
NP_063928.1	Mm.41213	2.17	NP_062570 .1	ATP-binding cassette, sub-family B, member 9 isoform 2	1294	0
			AAH17348. 1	Similar to ATP-binding cassette, sub-family B (MDR/TAP), member 9	1068	0
			BAC11171. 1	unnamed protein product	882	0
			BAA96044. 1	KIAA1520 protein	488	1.0e-137

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			BAB71769. 1	ABC-transporter	472	1.0e-132
			CAA80522. 1	TAP2B	471	1.0e-132
			AAC12903. 1	peptide transporter	471	1.0e-132
			AAC12905. 1	peptide transporter	471	1.0e-132
			NP_000535 .2	transporter 2, ATP-binding cassette, sub-family B isoform 1; transporter 2, ABC (ATP binding cassette); ATP-binding cassette, sub-family B (MDR/TAP), member 3; antigen peptide transporter 2; peptide supply factor 2; peptide transporter PSF2; ABC transporter, MHC 2	471	1.0e-132
			AAC12906. 1	peptide transporter	468	1.0e-131
			Q03518	Antigen peptide transporter 1 (APT1) (Peptide transporter TAP1) (Peptide transporter PSF1) (Peptide supply factor 1) (PSF-1) (Peptide transporter involved in antigen processing 1).	468	1.0e-131
			NP_000584 .2	transporter 1, ATP-binding cassette, sub-family B; ATP-binding cassette, sub-family B (MDR/TAP), member 2; antigen peptide transporter 1; ATP-binding cassette, sub-family B, member 2; transporter, ATP-binding cassette, major histocompatibility complex, 1; ABC transporter, MHC 1; peptide supply factor 1	468	1.0e-131
			AAA79901. 1	ABC transport protein	467	1.0e-131
			CAA80523. 1	TAP2E	466	1.0e-131
			Q03519	Antigen peptide transporter 2 (APT2) (Peptide transporter TAP2) (Peptide transporter PSF2) (Peptide supply factor 2) (PSF-2) (Peptide transporter involved in antigen processing 2).	466	1.0e-131

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			AAD31384. 1	transporter 2 isoform	437	1.0e-122
			NP_061313 .1	transporter 2, ATP-binding cassette, sub-family B isoform 2; transporter 2, ABC (ATP binding cassette); ATP-binding cassette, sub-family B (MDR/TAP), member 3; antigen peptide transporter 2; peptide supply factor 2; peptide transporter PSF2; ABC transporter, MHC 2	437	1.0e-122
			AAD23381. 1	TAP2 protein	403	1.0e-112
			AAD23601. 1	TAP2 protein	401	1.0e-111
			NP_036221 .1	ATP-binding cassette, sub-family B, member 10	397	1.0e-110
			BAB20265. 1	mono ATP-binding cassette protein	392	1.0e-108
			BAA92038. 1	unnamed protein product	363	1.0e-99
			BAC04392. 1	unnamed protein product	362	2.0e-99
			NP_009119 .1	ATP-binding cassette, sub-family B, member 8; mitochondrial ABC protein	357	6.0e-98
			Q9NUT2	ATP-binding cassette, sub-family B, member 8, mitochondrial precursor (Mitochondrial ATP-binding cassette 1) (M-ABC1).	357	6.0e-98
			AAA59575. 1	P-glycoprotein	321	4.0e-87
			CAD38811. 1	hypothetical protein	320	6.0e-87

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			NP_000918 .1	ATP-binding cassette, sub-family B (MDR/TAP), member 11; ABC member 16, MDR/TAP subfamily; progressive familial intrahepatic cholestasis 2; bile salt export pump	320	1.0e-86
			P08183	Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).	319	1.0e-86
			NP_000434 .1	ATP-binding cassette, subfamily B, member 4 isoform A; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	312	2.0e-84
			NP_061337 .1	ATP-binding cassette, subfamily B, member 4 isoform B; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	312	2.0e-84
			NP_061338 .1	ATP-binding cassette, subfamily B, member 4 isoform C; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3	312	2.0e-84
			O95342	Bile salt export pump (ATP-binding cassette, sub-family B, member 11).	311	3.0e-84
			AAD28285. 1	bile salt export pump	311	3.0e-84
			NP_003733 .2	ATP-binding cassette, sub-family B (MDR/TAP), member 11; ABC member 16, MDR/TAP subfamily; progressive familial intrahepatic cholestasis 2; bile salt export pump	311	3.0e-84
			AAD50509. 1	TAP2 protein	308	2.0e-83
			CAA40740. 1	Y3	292	2.0e-78
			1703419A	MHC II Y3 gene	292	2.0e-78

220

				AAN76500. 1	P-glycoprotein	270	7.0e-72
				CAA29547. 1	P-glycoprotein (431 AA)	254	7.0e-67
				1JJ7 A	Chain A, Crystal Structure Of The C-Terminal Atpase Domain Of Human Tap1	247	6.0e-65
				AAG33617. 1	ATP-binding cassette, sub-family B (MDR/TAP), member 11; ABC member 16, MDR/TAP subfamily; progressive familial intrahepatic cholestasis 2; bile salt export pump	229	1.0e-59
				NP_005680 .1	ATP-binding cassette, sub-family B, member 6	229	1.0e-59
				BAB71347. 1	unnamed protein product	226	2.0e-58
				AAC28653. 1	ABC transporter	224	6.0e-58
				AAH06323. 1	ATP-binding cassette, sub-family B (MDR/TAP), member 7	208	3.0e-53
				O75027	ATP-binding cassette, sub-family B, member 7, mitochondrial precursor (ATP-binding cassette transporter 7) (ABC transporter 7 protein).	208	3.0e-53
				AAD47141. 1	ABC transporter	207	7.0e-53
				NP_004290 .1	ATP-binding cassette, sub-family B, member 7; ATP-binding cassette 7	206	2.0e-52
				BAA28861. 1	ABC transporter 7 protein	206	2.0e-52
NM_007471				CAA68374. 1	precursor polypeptide (AA 1-695)	1112	0
NP_031497.1	Mm.15571	U:(C-D)+ 2.16					

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221

			CAA31830. 1	A4 amyloid protein precursor	1111	0
			1507304B	beta amyloid peptide precursor	886	0
			1507304A	beta amyloid peptide precursor	736	0
			NP_000475 .1	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease); Amyloid beta (A4) precursor protein; amyloid beta-peptide	736	0
			CAA30050. 1	amyloid A4 protein	736	0
			AAA51722. 1	amyloid beta-protein precursor	735	0
			AAA51726. 1	beta-amyloid A4	469	1.0e-132
			AAB59501. 1	amyloid-beta protein	400	1.0e-111
			AAH04369. 1	APP protein	400	1.0e-111
			AAA58727. 1	amyloid precursor protein	379	1.0e-104
			AAA35601. 1	binding protein	351	3.0e-96
			AAH00373. 1	Similar to amyloid beta ...	351	3.0e-96
			AAA36032. 1	binding protein	351	3.0e-96
			AAH04371. 1	Unknown (protein for MGC:10449)	350	7.0e-96
			AAD47291. 1	amyloid precursor protein homolog HSD-2	349	9.0e-96

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				3HADA	Chain A, Biochemical Characterization And Structure Determination Of Human Heart Short	526	1.0e-149
				1F12A	Chain L-3-Hydroxyacyl CoA Dehydrogenase Provide Insight Into Catalytic Mechanism.	525	1.0e-149
				2HDHA	Chain A, L-3-Hydroxyacyl-CoA Dehydrogenase Complexed With 3-Hydroxybutyryl-CoA.	506	1.0e-143
					Chain A, Biochemical Characterization And Structure Determination Of Human Heart Short		
					Chain L-3-Hydroxyacyl CoA Dehydrogenase Provide Insight Into Catalytic Mechanism.		
					growth arrest-specific 6; AXL stimulatory factor	1075	0
					protein S (alpha); Protein S, alpha	550	1.0e-155
					Vitamin K-dependent protein S precursor	549	1.0e-155
					protein S alpha	548	1.0e-154
					protein S precursor	542	1.0e-152
					pre-protein S (AA -15 to 635)-ttg start	541	1.0e-152
					Down syndrome critical region protein 3; Down syndrome critical region protein A	524	1.0e-148
					Down syndrome critical protein A - human	519	1.0e-147
					hypothetical protein	334	2.0e-91
					Dimethylalanine monooxygenase [N-oxide forming] 3 (Hepatic flavin-containing monooxygenase 3) (FMO 3) (Dimethylalanine oxidase 3) (FMO form 2) (FMO II).	847	0
					Flavin containing monooxygenase 3	847	0
					dimethylalanine monooxygenase (N-oxide-forming) (EC 1.14.13.8) 3	846	0
					dimethylalanine monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 2	795	0
					Putative dimethylalanine monooxygenase [N-oxide forming] 6 (Flavin-containing monooxygenase 6) (FMO 6) (Dimethylalanine oxidase 6).	770	0
					Dimethylalanine monooxygenase [N-oxide forming] 2 (Pulmonary flavin-containing monooxygenase 2) (FMO 2) (Dimethylalanine oxidase 2) (FMO 1B1).	610	1.0e-174
					flavin containing monooxygenase 1; Flavin-containing monooxygenase 1 (fetal liver)	580	1.0e-165

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				NP_001451	flavin containing monooxygenase 2; Flavin-containing monooxygenase 2 (adult liver)	561	1.0e-160
				P49326	Dimethylalanine monooxygenase [N-oxide forming] 5 (Hepatic flavin-containing monooxygenase 5) (FMO 5) (Dimethylalanine oxidase 5).	546	1.0e-155
				NP_001452	flavin containing monooxygenase 5	545	1.0e-155
				NP_002013	flavin containing monooxygenase 4	533	1.0e-151
				AAH35687	Similar to flavin containing monooxygenase 5	300	5.0e-81
				BAB13975	unnamed protein product	300	6.0e-81
				XP_060711	similar to dimethylalanine monooxygenase	205	2.0e-52
NM_009073							
			U:(C-D)+				
NP_033099.1	Mm.679	2.13	NP_000318	retinal outer segment membrane protein 1; rod outer segment membrane protein 1	424	1.0e-118	
NM_020568							
			U:(C-D)+				
NP_065593.1	Mm.12966	2.12	BAB67774	KIAA1881 protein	1524	0	
			XP_170901	similar to KIAA1881 protein	248	5.0e-65	
NM_033327							
			U:(C-D)+				
NP_201584.1	Mm.23452	2.12	NP_055884	OLF-1/EBF associated zinc finger protein; Smad- and Olf-interacting zinc finger protein	2356	0	
			NP_056276	early hematopoietic zinc finger	1563	0	
			BAB84872	FLJ00107 protein	1561	0	
			AAH32869	Similar to early hematopoietic zinc finger	1560	0	
			CAD57322	early hematopoietic zinc finger	1553	0	
			BAB13829	unnamed protein product	1030	0	
			TI7326	hypothetical protein DKFp564D0764.1 - human (fragment).	887	0	
			AAG49442	LYST-interacting protein LIP3	275	5.0e-73	
			NP_003421	zinc finger protein 91 (HPF7, HTF10)	253	2.0e-66	
			NP_009084	zinc finger protein 208	233	2.0e-60	

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				AAH07307	Similar to zinc finger protein 268	212	4.0e-54
NM_010902							
NP_035032.1	Mm.1025	U:(C-D)+ 2.11		NP_006155 I59340	nuclear factor (erythroid-derived 2)-like 2 transcription factor Nr2f2	904	0
				BAC03440	FLJ00380 protein	870	0
				NP_003195	nuclear factor (erythroid-derived 2)-like 1; transcription factor 11 (basic leucine zipper type)	295	2.0e-79
				A49672	transcription factor Nrfl	295	2.0e-79
				AAA20466	transcription factor LCR-F1.	273	1.0e-72
						225	2.0e-58
NM_010217							
NP_034347.1	Mm.1810	U:(C-D)+ 2.1		NP_001892.	connective tissue growth factor	670	0
				CAC44023	bA6918.1 (connective tissue growth factor)	667	0
				AAA75378	connective tissue growth factor	586	1.0e-167
				AAH15028	nephroblastoma overexpressed gene	374	1.0e-103
				NP_002505	nov precursor	374	1.0e-103
				AAG59863	CYR61 protein	343	4.0e-94
					CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (GIG1 protein).		
				O00622		342	1.0e-93
				CAA72167	CYR61 protein	341	3.0e-93
				AAB84227	Cyr61 protein	341	3.0e-93
					WNT1 inducible signaling pathway protein 1 isoform 1 precursor; wnt-1 signaling pathway protein 1; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1		
				NP_003873	tumor RMS cell line RD specific product	305	2.0e-82
				AAF21597		259	1.0e-68
					WNT1 inducible signaling pathway protein 3 isoform 2; wnt-1 signaling pathway protein 3; Wnt1 signaling pathway protein 3; Wnt-1 inducible signaling pathway protein 3		
				NP_569080		249	1.0e-65
					WNT1 inducible signaling pathway protein 3 isoform 1; wnt-1 signaling pathway protein 3; Wnt1 signaling pathway protein 3; Wnt-1 inducible signaling pathway protein 3		
				NP_003871		249	1.0e-65

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				NP_003872	WNT1 inducible signaling pathway protein 2 precursor; wnt-1 signaling pathway protein 2; connective tissue growth factor-like protein	199	1.0e-50
NM_011812				NP_006320	fibulin 5 precursor; urine p50 protein; developmental arteries and neural crest epidermal growth factor-like	869	0
NP_035942.1	Mm.25347	U:(C-D)+ 2.1		AAC62107.1	UP50	859	0
				CAD62618.1	unnamed protein product	856	0
				CAA10791.2	fibulin-4	476	1.0e-133
				O95967	EGF-containing fibulin-like extracellular matrix protein 2 precursor (Fibulin-4) (FIBL-4) (UPH1 protein).	476	1.0e-133
				NP_058634.1	EGF-containing fibulin-like extracellular matrix protein 2; fibulin 4	474	1.0e-133
				AAG45245.1	fibulin-like extracellular matrix protein	468	1.0e-131
				AAC62108.1	PH1	456	1.0e-127
				NP_004096.2	EGF-containing fibulin-like extracellular matrix protein 1 isoform a precursor; fibrillin-like	374	1.0e-102
				I38449	extracellular protein - human	374	1.0e-102
				NP_061489.1	EGF-containing fibulin-like extracellular matrix protein 1 isoform b; fibrillin-like	374	1.0e-102
				CAB43267.1	hypothetical protein	273	1.0e-72
				AAN05435.1	fibulin 2	273	2.0e-72

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				NP_001989 .1	fibulin 2 precursor; Fibulin-2	273	3.0e-72
				AAN05436. 1	fibulin 2	273	3.0e-72
				AAH22497. 1	fibulin 1	265	5.0e-70
				NP_001987 .1	fibulin 1 isoform C precursor	265	5.0e-70
				BAC11705. 1	unnamed protein product	242	4.0e-63
				NP_006477 .1	fibulin 1 isoform D	242	5.0e-63
				AAG17241. 1	unknown	241	6.0e-63
				NP_006476 .1	fibulin 1 isoform B precursor	223	2.0e-57
				NP_006478 .1	fibulin 1 isoform A precursor	223	2.0e-57
NM_011693 NP_035823.1	Mm.1021	U:(C-D)+ 2.08		NP_001069.1	vascular cell adhesion molecule 1, isoform a precursor; CD106 antigen	1132	0
				NP_542413.1	vascular cell adhesion molecule 1, isoform b precursor; CD106 antigen	573	1.0e-162
				pdj1VCA	Human Vascular Cell Adhesion Molecule-1; Chain: A, B; Synonym: Vcam-D1,2	303	7.0e-81
				pdj1IJ9	Vascular Cell Adhesion Protein 1; Chain: A; Fragment: Vcam-D1, D2 (Integrin Binding Fragment); Synonym: Vcam-1	293	1.0e-77
				pdj1VSC	Vascular Cell Adhesion Molecule-1; Chain: A, B; Fragment: N-Terminal Two-Domain Fragment; Synonym: Vcam-1; Engineered: Yes; Mutation: Y196D; Other_Details: Hybrid Molecule Composed Of Vcam-1 Domains 1 and 2 Fused To IgG, Hinge and Fc	290	8.0e-77

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NM_011391			U:(C-D)+				
NP_035521.1	Mm.29161	2.08	O60669	Monocarboxylate transporter 2 (MCT 2).	636	0	
				solute carrier family 16 (monocarboxylic acid transporters), member 7; monocarboxylate transporter 2	636	0	
			NP_004722		632	0	
			AAC70919	monocarboxylate transporter 2; MCT2	525	1.0e-148	
			CAD27707	monocarboxylate transporter isoform 1	525	1.0e-148	
			NP_003042.	solute carrier family 16 (monocarboxylic acid transporters), member1	525	1.0e-148	
			A55568	monocarboxylate transporter 1 - human	525	1.0e-148	
				solute carrier family 16 (monocarboxylic acid transporters), member 3; monocarboxylate transporter 3	366	1.0e-101	
			NP_004198		365	1.0e-100	
			O95907	Monocarboxylate transporter 3 (MCT 3).	363	1.0e-100	
			NP_037488	solute carrier 16 (monocarboxylic acid transporters), member 8; monocarboxylate transporter 3			
				solute carrier family 16 (monocarboxylic acid transporters), member 5; monocarboxylate transporter 5	280	6.0e-75	
			NP_004686		211	4.0e-54	
			NP_699188	hypothetical protein FLJ90193			
NM_010225							
			U:(C-D)+				
NP_034355.1	Mm.6260	2.08	NP_001443	forkhead box F2; forkhead (Drosophila)-like 6	521	1.0e-147	
			2208384B	transcription factor FREAC-2	508	1.0e-143	
				forkhead box F1; forkhead (Drosophila)-like 5; Forkhead, drosophila, homolog-like 5; forkhead-related activator 1	251	2.0e-66	
			NP_001442				
NM_011851							
			U:(C-D)+				
NP_035981.1	Mm.56948	2.08	NP_002517	5' nucleotidase, ecto; Purine 5-Prime-Nucleotidase; 5' nucleotidase (CD73);	996	0	
			AAH15940	ecto-5'-nucleotidase	409	1.0e-113	
			AAC98672	NT5E protein	257	9.0e-68	
				ecto-5'-nucleotidase			

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[illegible]

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NP_002631			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)	391	e-108
.1					
NP_109591			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2	362	1.0e-99
.1			(anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived		
1BY7A			Chain A, Human Plasminogen Activator Inhibitor-2. Loop (66-98) Deletion Mutant	310	3.0e-84
NP_002965			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4; protease inhibitor (leucine-serpin); squamous cell carcinoma antigen 2; leupin	306	6.0e-83
.1					
I38202			leupin precursor - human	305	1.0e-82
I38201			squamous cell carcinoma antigen 1 - human	303	5.0e-82
NP_008850			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3; squamous cell carcinoma antigen 1	302	1.0e-81
.1					
AAB20405.			squamous cell carcinoma antigen; SCC antigen	301	2.0e-81
1					
CAD56658.			squamous cell carcinoma antigen 1	300	3.0e-81
1					
NP_002566			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; plasminogen activator inhibitor, type II (arginine-serpin)	300	6.0e-81
.1					
AAH12609.			Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	296	5.0e-80
1					
AAA36413.			plasminogen activator inhibitor	295	1.0e-79
1					
NP_005015			serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)	295	2.0e-79
.1					
AAO15303.			MSTP057	291	3.0e-78
1					

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			BAB40773. 1	SCCA2b		284	3.0e-76
			JC7118	headpin serine proteinase inhibitor		276	5.0e-74
			CAA04937. 1	hurpin		276	5.0e-74
			NP_036529 .1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13; hurpin; protease inhibitor 13 (hurpin, headpin)		276	7.0e-74
			NP_536722 .1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12	271	3.0e-72	
			NP_002630 .1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5; protease inhibitor 5 (maspin)	266	7.0e-71	
			NP_536723 .1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 11	263	6.0e-70	
			AAL16057. 1	serine proteinase inhibitor SERPINB11	263	6.0e-70	
			Q96P15	Serpin B11	263	8.0e-70	
			AAH34528. 1	Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8	240	6.0e-63	
			BAB40772. 1	SCCA1b	238	2.0e-62	
			NP_003775 .1	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7; mesangium predominant gene, megsin	233	9.0e-61	
			CAC03569. 1	hurpin	219	1.0e-56	
			1IZ2A	Chain A, Interactions Causing The Kinetic Trap In Serpin Protein Folding	216	7.0e-56	
			1313184B	alpha1 antitrypsin	216	9.0e-56	
			1HP7A	Chain A, A 2.1 Angstrom Structure Of An Uncleaved Alpha-1-Antitrypsin Shows Variability Of The Reactive Center And Other Loops.	213	7.0e-55	

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			1ATU	Uncleaved Alpha-1-Antitrypsin	212	2.0e-54
			1KCT	Alpha-1-Antitrypsin	212	2.0e-54
			1012287A	antitrypsin alpha1 mutant	211	2.0e-54
			AAB60386.1	protein C inhibitor	210	6.0e-54
			1ATHA	Chain A, Antithrombin Iii	209	8.0e-54
			1ATHB	Chain B, Antithrombin Iii	209	8.0e-54
			NP_000479.1	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1; antithrombin III	209	8.0e-54
			BAA06212.1	antithrombin III variant	209	1.0e-53
			AAH15642.1	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	208	2.0e-53
			1PSI	Intact Recombined Alpha-1-Antitrypsin Mutant Phe 51 To Leu	208	2.0e-53
			P01009	Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (PRO0684/PRO2209).	208	2.0e-53
			1QLPA	Chain A, 2.0 Angstrom Structure Of Intact Alpha-1-Antitrypsin: A Canonical Template For Active Serpins	208	2.0e-53
			NP_000286.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	207	3.0e-53
			AAA51547.1	alpha-1-antitrypsin precursor	207	5.0e-53
			1DZHI	Chain I, P14-Fluorescein-N135q-S380c-Antithrombin-Iii	207	5.0e-53
			CAB45766.1	hypothetical protein	207	5.0e-53

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			NP_000615.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)	207	5.0e-53
			1DZGI	Chain I, N135q-S380c-Antithrombin-III	206	7.0e-53
			AAA51546.1	alpha-1-antitrypsin	206	9.0e-53
			AAB26244.2	acrosomal serine protease inhibitor	206	9.0e-53
			AAA51796.1	antithrombin III	206	1.0e-52
			AAF29581.1	PRO0684	205	2.0e-52
			AAB59495.1	alpha-1-antitrypsin	205	2.0e-52
			AAA35688.1	plasma serine protease inhibitor precursor	204	4.0e-52
			AAA51560.1	alpha-1-antichymotrypsin precursor	197	3.0e-50
			P01011	Alpha-1-antichymotrypsin precursor (ACT).	197	3.0e-50
			AAD08810.1	alpha-1-antichymotrypsin precursor	197	3.0e-50
			CAA48671.1	alpha1-antichymotrypsin	197	3.0e-50
			AAH34554.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	197	4.0e-50
			1LQ8A	Chain A, Crystal Structure Of Cleaved Protein C Inhibitor	196	7.0e-50
			1QMNA	Chain A, Alpha1-Antichymotrypsin Serpin In The Delta Conformation (Partial Loop Insertion).	196	9.0e-50

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				7APIA	Chain A, Modified Alpha1-Antitrypsin (Modified Alpha1-Proteinase Inhibitor) (Tetragonal Form 1).	196	9.0e-50
				1D5SA	Chain A, Crystal Structure Of Cleaved Antitrypsin Polymer	196	9.0e-50
NM_008880							
NP_032906.1	Mm.10306	U:(C-D)+ 2.06		NP_066928	phospholipid scramblase 1	428	1.0e-119
				NP_065092	phospholipid scramblase 2	357	2.0e-98
				NP_065086	phospholipid scramblase 4	263	4.0e-70
				AAH28354	phospholipid scramblase 4	263	6.0e-70
				Q9NRY6	Phospholipid scramblase 3 (PL scramblase 3) (Ca(2+)-dependent phospholipid scramblase 3).	258	1.0e-68
				BAC11458	unnamed protein product	258	1.0e-68
				AAH11735	Similar to phospholipid scramblase 3	257	3.0e-68
NM_008796							
NP_032822.1	Mm.5062	U:(C-D)+ 2.05		Q9UKL6	Phosphatidylcholine transfer protein (PC-TP) (StAR-related lipid transfer protein 2) (StARD2) (START domain-containing protein 2).	361	1.0e-100
				NP_067036	phosphatidylcholine transfer protein; START domain containing 2	359	3.0e-99
				AAF08345	phosphatidylcholine transfer protein	356	2.0e-98
					Chain A, Crystal Structure Of Human Phosphatidylcholine Transfer Protein In Complex With		
				1LN2A.	Dilinoleoylphosphatidylcholine (Seleno-Met Protein).	352	2.0e-97
				AAH05112	Unknown (protein for IMAGE:4026343)	295	5.0e-80
NM_011676	Mm.27744	U:(C-D)+ 2.04		NP_005139.1	unc119 (C.elegans) homolog, isoform a; unc119 (C.elegans) homolog; retinal protein 4		
NP_035806.1				NP_473376.1	unc119 (C.elegans) homolog, isoform b; unc119 (C.elegans) homolog; retinal protein 4	391	1.0e-108
NM_011717						317	2.0e-85
NP_035847.1	Mm.20878	U:(C-D)+ 2.04		AAD19818	Human homolog of Mus musculus wizL protein [AA 4-1561]	1444	0
				AAD19817	Human homolog of Mus musculus wizS protein [AA 64-934]	1443	0

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				AAC97985	Human homolog of Mus musculus wizS protein [AA 171-934]	1223	0
				XP_086045	widely-interspaced zinc finger motifs	1223	0
				:BAB55234	unnamed protein product	758	0
				AAH07551	WIZ protein	562	1.0e-159
				T51885	hypothetical protein DKFZp547M136.1 - human (fragment).	215	3.0e-55
				AAH02329	Unknown (protein for IMAGE:3532992)	210	1.0e-53
NM_009197							
					solute carrier family 16 (monocarboxylic acid transporters), member 2; X-linked		
			U:(C-D)+		PEST-containing transporter	814	0
NP_033223.1	Mm.5045	2.04		NP_006508		814	0
				AAB60374	X-linked PEST-containing transporter		
					solute carrier family 16 (monocarboxylic acid transporters), member 10; T-type amino acid transporter 1		
				NP_061063		453	1.0e-126
				AAF71072	PRO0813	200	1.0e-40
				AAH17968	hypothetical protein PRO0813	199	3.0e-50
NM_009632							
			U:(C-D)+				
NP_033762.1	Mm.5728	2.04		CAB65088	poly-(ADP-ribose) polymerase II	987	0
					Poly [ADP-ribose] polymerase-2 (PARP-2) (NAD(+) ADP-ribosyltransferase-2)		
				Q9UGN5	(Poly[ADP-ribose] synthetase-2) (pADPRT-2) (hPARP-2).	982	0
				CAB41505	poly(ADP-ribose) polymerase-2	942	0
					poly (ADP-ribose) transferase-like 2; ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 2; poly(ADP-ribose) synthetase		
				NP_005475		939	0
				BAA92017	unnamed protein product	877	0
				AAA51599	poly(ADP-ribose) polymerase	382	1.0e-106
				AAB59447	poly(ADP-ribose) synthetase.	381	1.0e-105
					Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase-1)		
				P09874	(Poly[ADP-ribose] synthetase-1).	381	1.0e-105
				AAA60137	poly(ADP-ribose) polymerase	381	1.0e-105

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				AAH37545	ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)	380	1.0e-105
				NP_001609	poly(ADP-ribose)transferase; ADP-ribosyltransferase NAD(+); poly(ADP-ribose) synthetase	379	1.0e-105
				AAH14260	Unknown (protein for MGC:20611)	274	2.0e-73
				AAM95460	poly (ADP-ribose) polymerase 3	274	2.0e-73
					poly (ADP-ribosyl) transferase-like 3; ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)-like 2; poly(ADP-ribose) synthetase	272	9.0e-73
				NP_005476		256	8.0e-68
				T08713	NAD ⁺ ADP-ribosyltransferase homolog DKFZp566G0224.1		
AF241249	Mm.35241	U:(C-D)+ 2.03		AAH23549.1	Unknown (protein for MGC:16590)	788	0
AAG02285.1				AAH07570.1	Unknown (protein for IMAGE:3029289)	628	1.0e-178
				BAB84871.1	FLJ00103 protein	516	1.0e-144
				XP_036104.4	similar to FLJ00103 protein	504	1.0e-141
				AAH12332.1	Unknown (protein for MGC:20519)	430	1.0e-118
				BAB47492.1	KIAA1863 protein	396	1.0e-109
				BAB71400.1	unnamed protein product	303	2.0e-80
NM_011176				NP_068813	matriptase; suppression of tumorigenicity 14 (colon carcinoma);	1484	0
		U:(C-D)+ 2.03		.1	membrane-type serine protease; serine protease TADG-15; tumor		
NP_035306.2	Mm.37947				associated differentially expressed gene 15 protein		
				BAB20376.1	prostamin	1483	0
				AAG15395.1	serine protease TADG15	1482	0
				AAH05826.1	Similar to suppression o...	983	0
				AAH18146.1	ST14 protein	799	0
				AAG13949.1	serine protease SMC19	618	1.0e-176

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			1EAWA	Chain A, Crystal Structure Of The Mtsp1 (Matriptase) -Bpt1 (Aprotinin) Complex	448	1.0e-125
			NP_705837.1	type II transmembrane serine protease 6; membrane-bound mosaic serine proteinase matriptase-2	418	1.0e-116
			CAC85953.1	matriptase-2	417	1.0e-116
			NP_002763.1	enterokinase precursor; proenterokinase; enteropeptidase	233	1.0e-60
			BAA95557.1	enterokinase	231	6.0e-60
			NP_054777.1	DESC1 protein	220	1.0e-56
			Q9Y5Q5	Atrial natriuretic peptide-converting enzyme (pro-ANP-converting enzyme) (Corin) (Heart specific serine proteinase ATC2).	214	1.0e-54
			AAK53559.1	epitheliasin	206	3.0e-52
			AAK29280.1	androgen-regulated serine protease TMPRSS2 precursor	206	3.0e-52
			NP_005647.2	transmembrane protease, serine 2; epitheliasin	206	3.0e-52
			AAC51784.1	serine protease	204	1.0e-51
NM_008797						
NP_032823.1	U:(C-D)+		NP_000911	pyruvate carboxylase precursor	2115	0
	Mm.1845	2.03	P11498	Pyruvate carboxylase, mitochondrial precursor (Pyruvic carboxylase) (PCB).	2114	0
			AAB31500	pyruvate carboxylase; pyruvate:carbon dioxide ligase	2093	0
			NP_000273	Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor	362	2.0e-99

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					AAL66189	propionyl-CoA carboxylase alpha subunit		362	2.0e-99
					BAA99407	3-methylcrotonyl-CoA carboxylase biotin-containing subunit		362	2.0e-99
						methylcrotonyl-Coenzyme A carboxylase 1 (alpha); 3-methylcrotonyl-CoA carboxylase biotin-containing subunit		362	2.0e-99
					NP_064551	3-methylcrotonyl-CoA carboxylase biotin-containing subunit		359	1.0e-98
					AAK67986	acetyl-CoA carboxylase (EC 6.4.1.2)		207	1.0e-52
					S41121	acetyl-Coenzyme A carboxylase alpha		206	2.0e-52
					NP_000655				
NM_010220	Mm.15439	U:(C-D)+			NP_004108.1	FK506-binding protein 5; 51 kDa FK506-binding protein 5; 54 kDa progesterone receptor-associated immunophilin; T-cell FK506-binding protein; peptidylprolyl cis-trans isomerase; rotamase; FF1 antigen; HSP90-binding immunophilin		783	0
NP_034350.1	0	2.02						770	0
					AAA86245.1	FKBP54			
					NP_002005.1	FK506-binding protein 4; FK506-binding protein 4 (59kD); T-cell FK506-binding protein, 59kD; p59 protein; HSP binding immunophilin; peptidylprolyl cis-trans isomerase; rotamase; FK506 binding protein 4 (59kD)		498	1.0e-139
					XP_095921.1	similar to FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)		343	7.0e-93
					XP_172777.1	similar to FK506-binding protein 4 (Possible peptidyl-prolyl cis-trans isomerase FKBP4) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)		323	6.0e-87
					AAH02887.1	Similar to FK506-binding protein 4 (59kD)		323	1.0e-86
NM_016696	Mm.24193	U:(C-D)+			NP_002072.1	glypican 1 precursor		934	0
NP_057905.1		2.02						490	1.0e-137
					NP_005699.1	glypican 6 precursor		445	1.0e-123
					NP_001439.2	glypican 4		444	1.0e-123
					O75487	Glypican-4 precursor (K-glypican)		443	1.0e-123
					AAC69991.1	glypican-4		409	1.0e-112
					CAB39178.1	GPC4 (glypican 4)		362	3.0e-98
					XP_168232.2	similar to Glypican-2 precursor (Cerebroglycan) (HSPG M13)			

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NM_013648			U:(C-D)+	AAC14910	NSP-like 1		512	1.0e-145
NP_038676.1	Mm.24142	2.02		AAC32543	RTN2-B		468	1.0e-131
				AAC32544	RTN2-C		349	9.0e-96
				NP_005610	reticulon 2		349	9.0e-96
				AAH14244	Similar to reticulon 2		282	1.0e-75
				NP_066959	reticulon 1; neuroendocrine-specific protein		199	1.0e-50
				AAA59951	neuroendocrine-specific protein B		199	1.0e-50
				I60904	neuroendocrine-specific protein C - human		198	3.0e-50
				AAH00314	Similar to reticulon 1		198	3.0e-50
NM_013692	Mm.4292	U:(C-D)+		NP_005646.1	TGFB inducible early growth response		742	0
NP_038720.1		2.01					723	0
				A57531	EGR alpha transcription factor - human		265	3.0e-69
				NP_003588.1	TGFB inducible early growth response 2			
AK004865	Mm.10633	U:(C-D)+		NP_005509.1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial);		929	0
BAB23626.1		2			3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2		679	0
				AAA92674.1	HMG CoA synthase			
				NP_002121.1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble);		659	0
				S27197	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1		650	0
					hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform		629	1.0e-179
				BAC04559.1	unnamed protein product			
				XP_060842.1	similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase)		244	4.0e-63
					(3-hydroxy-3-methylglutaryl coenzyme A synthase)		240	1.0e-61
				AAA92673.1	HMG CoA synthase			
NM_019810	Mm.25237	U:(C-D)+		NP_000334.1	solute carrier family 5 (sodium/glucose cotransporter), member 1; Human Na+/glucose			
NP_062784.1		2			cotransporter 1 mRNA, complete cds; solute carrier family 5 (sodium/glucose transporter), member 1		1024	0

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			NP_055042.1	solute carrier family 5 (low affinity glucose cotransporter), member 4; solute carrier family 5 (neutral amino acid transporters, system A), member 4; low affinity sodium glucose cotransporter.	856	0
			1909123A	Na glucose cotransporter	709	0
			NP_003032.1	solute carrier family 5 (sodium/glucose cotransporter), member 2; solute carrier family 5 (sodium/glucose transporter), member 2	709	0
			AAL66409.1	sodium/glucose cotransporter	700	0
5			CAC00574.1	dJ1024N4.1 (novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1))	583	1.0e-165
			NP_443176.2	sodium/myo-inositol cotransporter 2; putative sodium-coupled cotransporter RkST1; homolog of rabbit KST1	575	1.0e-162
			AAK97053.1	putative sodium-coupled cotransporter RkST1	574	1.0e-162
			XP_064487.3	ilar to 597 aa protein related to Na/glucose cotransporters	540	1.0e-152
			CAB06090.2	fF65B7.1 (solute carrier family 5 (sodium/glucose cotransporter), member 1 (SGLT1, High Affinity Sodium-Glucose Cotransporter))	512	1.0e-143
			P53794	Sodium/myo-inositol cotransporter (Na(+)/myo-inositol cotransporter)	511	1.0e-143
10			NP_008864.1	solute carrier family 5 (inositol transporters), member 3; solute carrier family 5 (inositol transporter), member 3; human solute carrier family 5, member 3, Sodium/myo-inositol cotransporter; sodium/myo-inositol cotransporter 1	510	1.0e-143
			NP_689564.1	hypothetical protein FLJ25217	399	1.0e-110
			NP_006396.2	transmembrane 9 superfamily member 1; multispanning membrane protein (70kD); transmembrane protein 9 superfamily member 1	1091	0
15			O15321	Transmembrane 9 superfamily protein member 1 precursor (hMP70)	1081	0
			AAF21983.1	SM-11044 binding protein	313	1.0e-83
			XP_050993.1	similar to Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-Iso)	313	1.0e-83
			AAF98159.1	transmembrane protein TM9SF3	312	1.0e-83
			BAB55369.1	unnamed protein product	305	2.0e-81
			NP_055557.1	KIAA0255 gene product	291	2.0e-77
20			NP_064508.1	endomembrane protein emp70 precursor isolog	265	2.0e-69

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			NP_004791.1	transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2	265	2.0e-69
			BAA91362.1	unnamed protein product	248	4.0e-64
			BAC11232.1	unnamed protein product	227	7.0e-58
NM_007743			AAB69977.1	alpha2(I) collagen	706	0
NP_031769.1	Mm.4482	U:(C-D)+ 2	NP_000080.1	alpha 2 type I collagen; Collagen I, alpha-2 polypeptide; Collagen of skin, tendon and bone, alpha-2 chain	704	0
			CGHU2S	collagen alpha 2(I) chain precursor	699	0
			AAB93981.1	pro-alpha 2(I) collagen	699	0
			P08123	Collagen alpha 2(I) chain precursor	699	0
			CAA23761.1	procollagen (1 is 3rd base in codon)	685	0
			CAA39142.1	type I collagen	553	1.0e-157
			NP_149162.1	alpha 1 type II collagen isoform 2, preproprotein; collagen II, alpha-1 polypeptide; cartilage collagen; chondrocalcin, included; COL11A3, formerly	458	1.0e-128
			P02458	Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin].	458	1.0e-128
			NP_001835.2	alpha 1 type II collagen isoform 1; collagen II, alpha-1 polypeptide; cartilage collagen; chondrocalcin, included; COL11A3, formerly	458	1.0e-128
			CGHU6C	collagen alpha 1(II) chain precursor [validated]	458	1.0e-128
			CGHU1S	collagen alpha 1(I) chain precursor	448	1.0e-125
			P02452	Collagen alpha 1(I) chain precursor	445	1.0e-124
			AAB94054.2	pro alpha 1(I) collagen	445	1.0e-124

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			NP_000079 .1	alpha 1 type I collagen preproprotein; Collagen I, alpha-1 polypeptide; osteogenesis imperfecta type IV; collagen of skin, tendon and bone, alpha-1 chain	442	1.0e-123
			AAA51995. 1	alpha 1 (I) chain propeptide	441	1.0e-123
			AAH36531. 1	Unknown (protein for MGC:33668)	439	1.0e-122
			AAA51997. 1	collagen alpha-1(II)	417	1.0e-116
			NP_000081 .1	alpha 1 type III collagen; Collagen III, alpha-1 polypeptide; collagen, fetal	394	1.0e-109
			CGHU7L	collagen alpha 1(III) chain precursor	393	1.0e-109
			CAA29886. 1	alpha1 (III) collagen	384	1.0e-106
			CAA28454. 1	pro- alpha (V)collagen (AA 1099)	359	2.0e-98
			NP_000384 .1	alpha 2 type V collagen preproprotein; Collagen V, alpha-2 polypeptide; AB collagen; collagen, fetal membrane, A polypeptide	359	2.0e-98
			AAL13166. 1	type V preprocollagen alpha 2 chain	357	7.0e-98
			AAH28178. 1	Similar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	352	2.0e-96
			CAA29604. 1	pro-alpha 1 (II) collagen (313 AA; AA 975-271c)	337	8.0e-92
			AAH43613. 1	Similar to collagen, type V, alpha 2	336	2.0e-91
			AAH07252. 1	Unknown (protein for MGC:15506)	335	4.0e-91

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			CAA26223. 1	pro alpha 1(II) collagen	333	1.0e-90
			AAA52002. 1	alpha-1 type III collagen	308	5.0e-83
			AAB27856. 1	type I collagen pro alpha 1(I) chain propeptide	303	1.0e-81
			CAA25879. 1	carboxy-propeptide of alpha 1 (III) procollagen	297	9.0e-80
			CAA29605. 1	C-terminal propeptide domain	291	4.0e-78
			AAA52058. 1	alpha-2 type V collagen	254	7.0e-67
			CAA68709. 1	prepro-alpha-2 chain	252	3.0e-66
			P12107	Collagen alpha 1(XI) chain precursor	214	1.0e-54
			CGHU1E	collagen alpha 1(XI) chain precursor	214	1.0e-54
			AAF04726. 1	collagen type XI alpha-a isoform B	213	1.0e-54
			NP_542196 .1	alpha 1 type XI collagen isoform B preproprotein; collagen XI, alpha-1 polypeptide	213	1.0e-54
			AAF04724. 1	collagen type XI alpha-1	213	1.0e-54
			NP_542197 .1	alpha 1 type XI collagen isoform C preproprotein; collagen XI, alpha-1 polypeptide	213	1.0e-54
			AAF04725. 1	collagen type XI alpha-1 isoform A	213	1.0e-54
			NP_001845 .2	alpha 1 type XI collagen isoform A preproprotein; collagen XI, alpha-1 polypeptide	213	1.0e-54
			NP_000084 .2	alpha 1 type V collagen preproprotein	206	2.0e-52

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				AAH08760.1	COL5A1 protein	206	2.0e-52
				1			
				P20908	Collagen alpha 1(V) chain precursor	206	2.0e-52
				CGH1V	collagen alpha 1(V) chain precursor	206	3.0e-52
				NP_071733.1	chromosome 11 open reading frame 24		
			U:(C-HI) +3.19				
			U:(C-D)+ 2.42				
5	AK007868					229	1.0e-58
	BAB25319.1	Mm.23780		AAH11765.1	chromosome 11 open reading frame 24	229	1.0e-58
10	NM_017480		U:(C-HI) +6.6	NP_036224.1	inducible T-cell co-stimulator; activation-inducible lymphocyte immunomodulatory molecule; inducible costimulator	264	3.0e-69
	NP_059508.1			AAH28006.1	Similar to inducible T-cell co-stimulator	216	1.0e-54
	M12571	Mm.19655	U:(C-HI) +3.58	NP_005336.2	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1	635	0
15	AA57234.1	9		P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)	635	0
				NP_005337.1	heat shock 70kDa protein 1B; heat shock 70kD protein 1B	633	1.0e-180
				A29160	dnaK-type molecular chaperone HSPA1L	628	1.0e-179
				XP_175177.1	heat shock 70kD protein 1-like	588	1.0e-167
				BAA32521.1	Heat shock protein 70 testis variant	586	1.0e-166
				NP_005518.1	heat shock 70kDa protein 1-like; Heat-shock 70kD protein-like-1	586	1.0e-166
				XP_166348.1	similar to heat shock protein	586	1.0e-166
				AAH34483.1	heat shock 70kD protein 1-like	585	1.0e-166
				NP_068814.2	heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2	567	1.0e-160
				AAH36107.1	Unknown (protein for MGC:33922)	567	1.0e-160
				NP_06588.1	Heat shock protein 70 testis variant	565	1.0e-160
				AAH07276.1	Similar to heat shock cognate 71-kd protein	565	1.0e-160
				AAD11466.1	heat shock protein	564	1.0e-159

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			AAH35665.1	heat shock 70kDa protein 6 (HSP70B')	555	1.0e-157
			NP_002146.1	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B'); Heat-shock 70kD protein-6 (HSP70B')	552	1.0e-156
NM_007585	Mm.584	U:(C-HI) +3.49, U:(C-D) 4.83	NP_004030.1	annexin A2; annexin II; lipocortin II; Annexin II (lipocortin I); calpactin I, heavy polypeptide (p36); annexin II (lipocortin II); calpactin I, heavy polypeptide); annexin II (lipocortin II)	654	0
NP_031611.1			AAH09564.1	annexin A2	653	0
			AAH23990.1	annexin A2	653	0
			CAB99342.1	bA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))	641	0
			NP_000691.1	annexin I; annexin I (lipocortin I); lipocortin I	335	8.0e-91
			pdb 1AIN	Annexin I	335	8.0e-91
			NP_001144.1	annexin IV; annexin IV (placental anticoagulant protein II); placental anticoagulant protein II	297	2.0e-79
			P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41)	297	2.0e-79
			AAC41689.1	protein PP4-X	297	2.0e-79
			NP_001148.1	annexin A11; annexin XI; autoantigen, 56-kD; calcyclin-associated annexin 50	294	2.0e-78
			NP_004024.1	annexin VI isoform 2; annexin VI (p68); calcium-binding protein p68; calphobindin II; protein p68 (1 - 673)	291	2.0e-77
			CAA68286.1	Annexin VI; Chain: A; Synonym: Lipocortin VI, P68, P70, Protein III, Chromobindin 20, 67 Kda Calelectrin, Calphobindin-II, Cpb- II	288	1.0e-76
			NP_001146.1	annexin VI isoform 1; annexin VI (p68); calcium-binding protein p68; calphobindin II; calelectrin F498	287	1.0e-76
			P08133	Annexin VI (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)	286	1.0e-76
			pdb 1AXN	Annexin III	281	1.0e-74

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				NP_005130.1	annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calmedin 35-alpha); calmedin 35-alpha	281	1.0e-74
				pdb 1HVD	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutation With Glu 17 Replaced By Gly (E17G)	274	2.0e-72
				NP_001145.1	annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoagulant protein I	274	2.0e-72
				pdb 1ANW	Annexin V	274	2.0e-72
				pdb 1HVF	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) Mutant With Glu 17 Replaced By Gly, Glu 78 Replaced By Gln (E17G, E78Q) Complexed With Calcium	273	4.0e-72
				AAH18671.1	annexin A5	273	5.0e-72
				pdb 1HVG	Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutant With Glu 78 Replaced By Gln (E78Q) (Second Crystal Form)	273	5.0e-72
				LUHU8	annexin VIII - human	271	1.0e-71
				NP_001621.1	annexin VIII; Annexin VII	271	1.0e-71
				pdb 1SAV	Annexin V; Chain: Null; Engineered: Yes; Mutation: P13, P87, P119, P163, and P248 Substituted With Thioproline (Prs); Biological_Unit: Monomer	271	1.0e-71
				XP_036593.2	similar to annexin A8	271	1.0e-71
				AAB46383.1	annexin VIII	265	1.0e-69
				NP_004025.1	annexin VII isoform 2; annexin VII (synexin); synexin	263	4.0e-69
				NP_001147.1	annexin VII isoform 1; annexin VII (synexin); synexin	262	9.0e-69
				XP_054475.4	similar to annexin A8	261	1.0e-68
				CAC34622.1	annexin A13 isoform b	257	3.0e-67
				NP_004297.1	annexin A13; annexin XIII; annexin, intestine-specific	252	9.0e-66
				AAH05830.1	Unknown (protein for MGC:1925)	248	2.0e-64
				AAG16780.1	keratinocyte annexin-like protein	245	1.0e-63
				NP_003559.1	annexin 31; annexin XXXI	245	1.0e-63

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NM_007980 NP_032006.1	Mm.28398	U:(C-HI) +3.49, U:(C-D) 2.22	NP_000125.1	intestinal fatty acid binding protein 2; Fatty acid-binding protein, intestinal; I-FABP; fatty acid binding protein 2, intestinal	219	2.0e-56
			pdbj3IFB	Intestinal Fatty Acid Binding Protein; Chain: A; Synonym: I-Fabp	218	7.0e-56
NM_007809 NP_031835.1	Mm.1262	U:(C-HI) +3.41, U:(C-D) 3.69	NP_000093.1	cytochrome P450, subfamily XVII polypeptide; steroid 17-alpha-monooxygenase; steroid 17-alpha-hydroxylase/17,20 lyase; cytochrome p450 XVIIA1		
			AAA59984.1	cytochrome P450c17	710	0
			AAA52140.1	steroid 17-alpha-hydroxylase	709	0
			CAA26458.1	cytochrome P(1)-450	706	0
			NP_000490.1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	248	2.0e-64
			AAA52139.1	cytochrome P-450-1	248	2.0e-64
			AAK25728.1	cytochrome P-450-1	246	9.0e-64
			NP_000752.1	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase	231	2.0e-59
			AAF13599.1	cytochrome P450-1A2	231	2.0e-59
			AAA35738.1	cytochrome P450 4	230	4.0e-59
			P08686	Cytochrome P450 XXIB (Steroid 21-hydroxylase) (P450-C21B)	229	9.0e-59
			AAA52063.1	CYP21B protein	228	2.0e-58
			NP_000491.2	cytochrome P450, subfamily XXIA polypeptide 2; steroid 21-monooxygenase; steroid 21-hydroxylase	226	6.0e-58
			AAA52064.1	21-hydroxylase B	226	6.0e-58
			AAA52065.1	mutant 21-hydroxylase B	226	6.0e-58
			CAA41709.1	steroid 21-monooxygenase	224	2.0e-57

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				AAC50809.1	cytochrome P450 CYP1B1		224	3.0e-57
				NP_000095.1	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase		224	3.0e-57
				AAB59440.1	steroid 21-hydroxylase		224	3.0e-57
AK007868	Mm.23780	U:(C-HI)		NP_071733.1	chromosome 11 open reading frame 24			
BAB25319.1		3.19, U:(C-D) 2.42					229	1.0e-58
				AAH11765.1	chromosome 11 open reading frame 24		229	1.0e-58
U67189	Mm.18170	U:(C-HI)		O15492	Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R) (A28-RGS14P)		323	2.0e-87
AAB50619.1	9	3.17		NP_002919.1	regulator of G-protein signalling 16; Regulator of G protein signaling-16		320	2.0e-86
M63245	Mm.19143	U:(C-HI)		NP_000679.1	aminolevulinic acid synthase 1		833	0
AAA91867.1		3.05		CAA68506.1	5-aminolevulinic acid synthase precursor		808	0
				CAB06076.1	5-aminolevulinic acid synthase		645	0
				P22557	5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinic acid synthase) (Delta-ALA synthetase) (ALAS-E)		645	0
				CAA39795.1	delta-aminolevulinic acid synthase (erythroid)		644	0
				NP_000023.1	aminolevulinic acid synthase 2; Aminolevulinic acid synthase-2		644	0
				AAH30230.1	Similar to aminolevulinic acid synthase 2 (sideroblastic/hypochromic anemia)		642	0
				AAG35538.1	PRO2399		350	3.0e-95
NM_007437	Mm.4210	U:(C-HI)		XP_045060.2	similar to fatty aldehyde dehydrogenase			
NP_031463.1		3.02		NP_000373.1	aldehyde dehydrogenase 3A2; aldehyde dehydrogenase 10; aldehyde dehydrogenase 3 family, member A2; fatty aldehyde dehydrogenase		751	0
				NP_000682.3	aldehyde dehydrogenase 3 family, member A1; aldehyde dehydrogenase, dimeric		751	0
					NADP-preferred; acetaldehyde dehydrogenase; ALDH, stomach type		572	1.0e-162
				P30838	Aldehyde dehydrogenase, dimeric NADP-preferred (ALDH class 3) (ALDHIII)		572	1.0e-162

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			A42584	aldehyde dehydrogenase [NAD(P)] (EC 1.2.1.5) 3 -	572	1.0e-162
			AAH04370.1	aldehyde dehydrogenase 3	572	1.0e-162
			BAC04239.1	unnamed protein product	473	1.0e-132
			NP_000685.1	aldehyde dehydrogenase 3B1; aldehyde dehydrogenase 7; aldehyde dehydrogenase 3 family, member B1	453	1.0e-126
			AAH33099.1	Similar to aldehyde dehydrogenase 3 family, member B1	431	1.0e-119
			NP_000686.1	aldehyde dehydrogenase 3B2; aldehyde dehydrogenase 8; aldehyde dehydrogenase 3 family, member B2	392	1.0e-107
			AAH07685.1	Similar to aldehyde dehydrogenase 3 family, member B2	391	1.0e-107
			BAC03897.1	unnamed protein product	390	1.0e-107
10	NM_022331 NP_071726.1	Mm.29151 U:(C-HI) 3.00, U:(C-D) 2.29	NP_055500.1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-Inducible gene	592	1.0e-168
			AAC09357.1	unknown	525	1.0e-147
			AAG17233.1	unknown	295	2.0e-78
			AAH09739.1	Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	218	2.0e-55
			NP_071768.2	hypothetical protein FLJ22313	216	1.0e-54
			AAB27103.1	TLS-CHOP		
	NM_007837 NP_031863.1	Mm.7549 U:(C-HI) 2.98, U:(C-D) 2.16			245	5.0e-64
			CAA63088.1	chimeric cDNA from Myxoid liposarcoma	244	1.0e-63
			NP_004074.2	DNA-damage-inducible transcript 3; C/EBP homologous protein; growth arrest- and DNA damage-inducible	220	1.0e-56
			JC1169	DNA-damage-inducible protein GADD153 - human	216	3.0e-55

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NM_007860 NP_031886.1	Mm.2774	U:(C-HI) 2.84, U:(C-D) 2.06	P49895	Type I iodothyronine deiodinase (Type-I 5'deiodinase) (DIOI) (Type 1 DI) (5DI)	417	1.0e-115
			NP_000783.2	thyroxine deiodinase type 1; 5DI; thyroxine deiodinase type I (selenoprotein)	409	1.0e-113
			AAH17955.1	Similar to deiodinase, iodothyronine, type I	207	4.0e-52
AK007378 BAB24997.1	Mm.35083	U:(C-HI) 2.77	NP_077016.1	hypothetical protein MGC4504	379	e-104
NM_011375 NP_035505.1	Mm.38248	U:(C-HI) 2.65, U:(C-D) 2.16	NP_003887.1	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase); ganglioside G(M3) Synthase	628	1.0e-179
			AAD14634.1	CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase	626	1.0e-178
			NP_006270.1	sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase)	213	2.0e-53
			AAI14347.1	Gal beta 1,3(4) GlcNAc alpha 2,3-sialyltransferase	202	2.0e-50
NM_007760 NP_031786.1	Mm.20396	U:(C-HI) 2.57, U:(C-D) 2.16	NP_000746.2	carnitine acetyltransferase precursor, isoform 1	1151	0
			P43155	Carnitine O-acetyltransferase (Carnitine acetylase) (CAT)	1139	0
			CAA55359.1	carnitine acetyltransferase	1124	0
			NP_003994.2	carnitine acetyltransferase isoform 2	1117	0
			NP_659006.1	carnitine acetyltransferase precursor, isoform 3	514	1.0e-144
			P28329	Choline O-acetyltransferase (CHOACTase) (Choline acetylase) (ChAT)	470	1.0e-131
			AAK08951.1	choline acetyltransferase isoform S	470	1.0e-131
			NP_065574.1	choline acetyltransferase isoform 2; acetyl CoA:choline O-acetyltransferase	468	1.0e-130
			AAK08952.1	choline acetyltransferase isoform R	468	1.0e-130
			NP_066266.1	choline acetyltransferase isoform 1; acetyl CoA:choline O-acetyltransferase	465	1.0e-129
			T01786	choline acetyltransferase - human (fragment).	409	1.0e-113

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NM_020570	Mm.14376	U:(C-HI)	NP_005422.1	X-ray repair cross complementing protein 2; X-ray repair, complementing defective, repair in Chinese hamster; DNA repair protein XRCC2	422	1.0e-117
NP_065595.1	7	2.55				
NM_019423	Mm.2567	U:(C-HI)	NP_060240.1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2		
NP_062296.1		2.53, U:(C-D)				
		2.08			554	1.0e-156
			CAB89418.1	dJ483K16.1.1 (novel protein (isoform 1))	369	1.0e-100
			NP_068586.1	homolog of yeast long chain polyunsaturated fatty acid elongation	367	1.0e-100
			NP_073563.1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4; Stargardt disease 3 (autosomal dominant)	262	3.0e-69
			CAC19496.1	dJ92C4.1 (novel protein, partly predicted by Fgenesh and Genscan)	259	1.0e-67
NM_031162	Mm.1224	U:(C-HI)	AAH25703.1	CD3Z antigen, zeta polypeptide (TIT3 complex)		
NP_112439.1		2.49			233	3.0e-60
			P20963	T-cell surface glycoprotein CD3 zeta chain precursor (T-cell receptor T3 zeta chain)	228	2.0e-58
			NP_000725.1	T-cell receptor zeta chain precursor	227	3.0e-58
			AAF34793.1	T-cell receptor zeta chain precursor	213	4.0e-54
NM_019699	Mm.38901	U:(C-HI)	NP_004256.1	fatty acid desaturase 2; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase		
NP_062673.1		2.46		(delta-6-desaturase)-like 2	842	0
			AAH09011.1	fatty acid desaturase 2	726	0
			AAG43192.1	p5327	717	0
			T08765	probable delta-6 fatty acid desaturase (EC 1.14.99.-) - human (fragment).	605	1.0e-172
			NP_068373.1	fatty acid desaturase 3; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase		
				(delta-6-desaturase)-like 3	598	1.0e+170
			BAC11182.1	unnamed protein product	575	1.0e-163
			BAB55103.1	unnamed protein product	575	1.0e-163
			NP_037534.2	fatty acid desaturase 1; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5 desaturase; delta-5 fatty acid desaturase	575	1.0e-163
			AAH07846.1	fatty acid desaturase 1	572	1.0e-162
			AAF70457.1	delta-5 fatty acid desaturase	572	1.0e-162
			BAC11229.1	unnamed protein product	570	1.0e-161

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			AAF29378.1	delta-5 desaturase	570	1.0e-161
			BAB55173.1	unnamed protein product	569	1.0e-161
			AAC23396.1	BC269730_1	315	1.0e-106
			BAB55167.1	unnamed protein product	327	3.0e-88
NM_023719	Mm.77432	U:(C-HI)	BAB18859.1	VDUP1		
NP_076208.1		2.36, U:(C-D) 2.42			761	0
			NP_006463.2	thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3	760	0
			XP_041721.2	similar to RIKEN cDNA 2410003C09 gene	326	1.0e-87
			AAH28704.1	Unknown (protein for IMAGE:4838787)	326	1.0e-87
			BAA92614.1	KIAA1376 protein	306	8.0e-82
			XP_033042.2	similar to hypothetical protein CLONE24945	304	5.0e-81
			NP_056498.1	hypothetical protein CLONE24945	256	2.0e-66
			AAH22516.1	Unknown (protein for MGC:26574)	254	5.0e-66
			AAD20053.1	Unknown	214	7.0e-54
NM_013760	Mm.27432	U:(C-HI)	NP_036460.1	DnaJ (Hsp40) homolog, subfamily B, member 9; microvascular endothelial		
NP_038788.1		2.34, U:(C-D) 2.1		differentiation gene 1; DKFZP564F1862 protein; endoplasmic reticulum DnaJ homolog 4	391	1.0e-107
			AAD08848.1	similar to putative microvascular endothelial differentiation gene 1; similar to X98993 (PID:g1771560)	298	2.0e-79
NM_023184	Mm.41389	U:(C-HI)	NP_054798.1	Kruppel-like factor 15; KKLf protein; kidney-enriched Kruppel-like factor		
NP_075673.1		2.34			624	1.0e-178
NM_018791	Mm.10375	U:(C-HI)	NP_004225.2	zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc		
NP_061261.1	0	2.32		finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)	919	0
			AAF88107.1	Hypothetical zinc finger-like protein	600	1e-17-
			AAF88103.1	zinc finger protein 226	588	1.0e-166
			Q9NYT6	Zinc finger protein 226	587	1.0e-166
			NP_057528.1	zinc finger protein 226; Kruppel-associated box protein	586	1.0e-166

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			AAF63030.1	Zinc finger protein ZNF45	576	1.0e-163
			NP_003416.1	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide); Zinc finger protein-45 (a Kruppel-associated box (KRAB) domain similar to Zinc finger protein 229	573	1.0e-162
			XP_091906.2		548	1.0e-155
			AAD12728.1	zinc finger protein	541	1.0e-152
			AAF76875.1	zinc finger protein	533	1.0e-150
5			NP_037530.1	zinc finger protein 224	518	1.0e-146
			NP_037512.1	zinc finger protein 228	517	1.0e-145
			XP_009363.3	similar to ZNF228 protein	515	1.0e-145
			AAG23968.1	ZNF228 protein	515	1.0e-145
			AAF88104.1	ZNF234	512	1.0e-144
10			XP_044207.1	similar to Zinc finger protein 234 (Zinc finger protein HZF4)	512	1.0e-144
			I37570	zinc finger protein - human (fragment)	511	1.0e-143
			Q14588	Zinc finger protein 234 (Zinc finger protein HZF4)	511	1.0e-143
			AAF24967.1	ZNF225	507	1.0e-142
			NP_653290.2	hypothetical protein FLJ32191	501	1.0e-140
			NP_037494.1	zinc finger protein 225	501	1.0e-140
			XP_084735.2	similar to RIKEN cDNA 1810054O13		
AK007864	Mm.27338	U:(C-HI)				
BAB25316.1		2.31			384	1.0e-105
			AAH17073	Similar to RIKEN cDNA 1810054O13 gene	346	7.0e-94
NM_019545	Mm.20413	U:(C-HI)	NP_057612.1	hydroxyacid oxidase 3; medium-chain 2-hydroxy acid oxidase HAOX3;		
NP_062418.1		2.31		(S)-2-hydroxy-acid oxidase; glycolate oxidase	645	0
			NP_057611.1	hydroxyacid oxidase 2; long-chain L-2-hydroxy acid oxidase; (S)-2-hydroxy-acid oxidase; glycolate oxidase		
			AAF14000.1	long-chain L-2-hydroxy acid oxidase	474	1.0e-132
			NP_060015.1	hydroxyacid oxidase 1; (S)-2-hydroxy-acid oxidase; glycolate oxidase	461	1.0e-128
			BAA82872.1	a liver-specific gene similar to the plant glycolate oxidase	300	3.0e-80
			NP_006197.1	platelet-derived growth factor receptor alpha precursor	299	8.0e-80
NM_011058	Mm.2924	U:(C-HI)				
NP_035188.1		2.3			1905	0

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				NP_002600.1	platelet-derived growth factor receptor beta precursor; beta platelet-derived growth factor receptor	826	0
				AAA36427.1	platelet-derived growth factor receptor	825	0
				AAH32224.1	platelet-derived growth factor receptor, beta polypeptide	825	0
				AAC50969.1	KIT protein	523	1.0e-146
				NP_000213.1	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog precursor	523	1.0e-146
				NP_005202.1	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	485	1.0e-135
				P07333	Macrophage colony stimulating factor I receptor precursor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen)	485	1.0e-135
				CAA81393.1	FLT3 receptor tyrosine kinase	414	1.0e-113
				NP_004110.1	fms-related tyrosine kinase 3	411	1.0e-113
				A36873	protein-tyrosine kinase (EC 2.7.1.112) STK-1 precursor - human	405	1.0e-111
				AAH15186.1	Unknown (protein for MGC:14519)	363	2.0e-98
				AAC16449.1	vascular endothelial growth factor receptor	352	3.0e-95
				NP_002010.1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	352	3.0e-95
				NP_002011.1	fms-related tyrosine kinase 4; fms-related tyrosine kinase-4 (vascular endothelial growth factor receptor 3)	344	1.0e-92
				CAA48290.1	FTL4	343	2.0e-92
				P35916	Vascular endothelial growth factor receptor 3 precursor (VEGFR-3) (Tyrosine-protein kinase receptor FLT4)	343	2.0e-92
				AAC16450.1	vascular endothelial growth factor receptor 2	341	7.0e-92
				NP_002244.1	kinase insert domain receptor (a type III receptor tyrosine kinase); Kinase insert domain receptor	341	7.0e-92
				JC1402	protein-tyrosine kinase (EC 2.7.1.112) KDR - human	340	1.0e-91
				I58357	receptor tyrosine kinase - human (fragment).	340	1.0e-91
NM_010565	Mm.2594	U:(C-HI)		NP_005529.1	inhibin beta C chain preproprotein; activin beta-C chain	503	1.0e+141
NP_034695.1		2.28		NP_113667.1	activin beta E	207	1.0e-52

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NM_011994	Mm.4817	U:(C-HI)	JC5712	adrenoleukodystrophy related protein		1353	0
NP_036124.1		2.27	NP_005155.1	ATP-binding cassette, sub-family D, member 2; adrenoleukodystrophy-like 1; hALDR		1348	0
			NP_000024.2	ATP-binding cassette, sub-family D (ALD), member 1; adrenoleukodystrophy protein		926	0
			1908394A	adrenoleukodystrophy protein		925	0
			P33897	Adrenoleukodystrophy protein (ALDP)		925	0
			AAB27045.1	70-kd peroxisomal membrane protein homolog {internal fragment} [human, Peptide Partial, 386 aa]		549	1.0e-155
			AAB00541.1	adrenoleukodystrophy related protein		510	1.0e-143
			NP_002849.1	ATP-binding cassette, sub-family D, member 3; Peroxisomal membrane protein-1 (70kD); peroxisomal membrane protein 1 (70kD, Zellweger syndrome); peroxisomal membrane protein-1		448	1.0e-124
			S20313	peroxisomal membrane protein, 70K - human		446	1.0e-124
			CAA58470.1	70kD peroxisomal integral membrane protein		406	1.0e-112
NM_018817	Mm.36676	U:(C-HI)	NP_054859.2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1; HepA-related protein; SMARCA-like protein 1		1213	0
NP_061287.1		2.27	AAH16482.1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1		1210	0
			AAF24984.1	HepA-related protein HARP		1205	0
			T34557	hypothetical protein DKFZp434B1050.1 - human (fragment)		1125	0
			BAA90955.1	unnamed protein product		975	0
			BAC04536.1	unnamed protein product		220	1.0e-55
AK006096	Mm.38305	U:(C-HI)	AAH11587.1	Similar to RIKEN cDNA 1700018O18 gene			
BAB24407.1		2.24	BAC04100.1	unnamed protein product		779	0
			AAH06353.1	Similar to RIKEN cDNA 1700018O18 gene		770	0
			XP_065744.2	similar to F16H11.1.p		550	1.0e-155
NM_019682	Mm.29908	U:(C-HI)	NP_003737.1	dynein, cytoplasmic, light polypeptide; Dynein, cytoplasmic, light chain (protein inhibitor of neuronal NOS); protein inhibitor of neuronal nitric oxide synthase		286	8.0e-76
NP_062656.1		2.24				188	3.0e-47

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NM_009154 NP_033180.1	Mm.24733	U:(C-HI) 2.23	NP_003957.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A; semaphorin F; sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, 5A	1993	0
			BAA95969.1	KIAA1445 protein	1243	0
			XP_032249.3	similar to KIAA1445 protein	1243	0
			AAC14668.1	semaphorin F	949	0
AK005274 BAB23924.1	Mm.19596 1	U:(C-HI) 2.22, U:(C-D) 2.15	NP_115680.1	hypothetical protein MGC2605		
			AAK61250.1	similar to HAGH	471	1.0e-131
			NP_005317.1	hydroxyacyl glutathione hydrolase; hydroxyacyl glutathione hydrolase 2; Hydroxyacyl glutathione hydrolase; glyoxalase II; hydroxyacylglutathione hydroxylase	376	1.0e-103
			BAB70814.1	unnamed protein product	266	6.0e-70
NM_009315 NP_033341.1	Mm.1994	U:(C-HI) 2.2	NP_005632.1	TBP-associated factor 6 isoform alpha; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	237	2.0e-69
			NP_620834.1	TBP-associated factor 6 isoform gamma; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	979	0
			NP_620835.1	TBP-associated factor 6 isoform delta; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit	957	0
NM_011361 NP_035491.1	Mm.28405	U:(C-HI) 2.2	AAD41091.1	serine/threonine protein kinase sgk	952	0
			NP_005618.1	serum/glucocorticoid regulated kinase	797	0
					796	0

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				AAH15326.1	Unknown (protein for MGC:21163)	532	1.0e-149
				AAF12758.1	protein kinase	532	1.0e-149
				NP_037389.2	serum/glucocorticoid regulated kinase-like; cytokine-independent survival kinase	527	1.0e-148
				AAF12757.2	protein kinase	506	1.0e-142
				NP_057360.2	serum/glucocorticoid regulated kinase 2 isoform beta	506	1.0e-142
				NP_005456.1	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B	327	4.0e-88
NM_011844	Mm.19479			NP_009214.1	monoglyceride lipase; lysophospholipase-like; likely ortholog of mouse monoglyceride lipase	538	1.0e-151
NP_035974.1	5	U:(C-HI) 2.19		CAC43316.1	monoglyceride lipase	528	1.0e-148
NM_018861	Mm.6379			AAA19438.1	neutral amino acid transporter	676	0
NP_061349.1		U:(C-HI) 2.18		NP_003029.2	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; Solute carrier family 1 (glutamate/neutral amino acid transporter),	676	0
				I55389	neutral amino acid transporter - human	673	0
				BAA94861.1	hASCT1	670	0
				A47131	Na+-dependent neutral amino acid transporter SATT	630	1.0e-179
				NP_005619.1	solute carrier family 1 (neutral amino acid transporter), member 5; baboon M7 virus receptor; RD114 virus receptor; neutral amino acid transporter B	365	2.0e-99
				AAD09814.1	neutral amino acid transporter	365	2.0e-99
				AAH00062.1	solute carrier family 1 (neutral amino acid transporter), member 5	365	2.0e-99
				AAK77026.1	sodium-dependent neutral amino acid transporter type 2 truncated isoform	365	2.0e-99
				AAC50629.1	neutral amino acid transporter B	365	3.0e-99
				AAD09812.1	RD114/simian type D retrovirus receptor	361	5.0e-98
AF213258	Mm.14976			NP_690864.1	membrane-associated guanylate kinase-related 3		
AAG43836	0	U:(C-HI) 2.17, U:(C-D) 2.34				1995	0
				XP_032749.2	similar to membrane-associated guanylate kinase MAGI3	1989	0

				AAG24545.1	membrane-associated guanylate kinase MAGI3	1972	0
				BAB13460.1	KIAA1634 protein	1590	0
				CAC17586.1	dJ730K3.2 (similar to BAI1-associated protein)	1163	0
				NP_036433.1	atrophin-1 interacting protein 1; activin receptor interacting p; KIAA0705 gene product	969	0
				AAK94066.1	MAGI-1C beta	853	0
				AAK94064.1	MAGI-1B alpha beta	847	0
				NP_004733.1	BAI1-associated protein 1; WW domain-containing protein 3	843	0
				JE0209	brain-specific angiogenesis inhibitor-associated protein 1 - human	839	0
				BAA31680.1	KIAA0705 protein	827	0
				AAK94065.1	MAGI-1A	689	0
				CAC36032.1	bA473L1.1 (novel protein similar to BAI1-associated protein 1 (BAIAP1))	587	1.0e-166
				BAB15479.1	unnamed protein product	300	1.0e-162
				AAC04844.1	membrane associated guanylate kinase 1	450	1.0e-125
NM_008382	Mm.3510	U:(C-HI)		NP_113667.1	activin beta E	537	1.0e-151
NP_032408.1		2.13		NP_005529.1	inhibin beta C chain preproprotein; activin beta-C chain	243	1.0e-62
NM_007679	Mm.4639	U:(C-HI)		NP_005186.1	CCAAAT/enhancer binding protein (C/EBP), delta	343	3.0e-93
NP_031705.1		2.11		A40225	transcription activator NF-IL6 beta - human	340	4.0e-92
				XP_171180.1	similar to CCAAT/enhancer binding protein delta (C/EBP delta) (Nuclear factor NF-IL6-beta) (NF-IL6-beta)	340	4.0e-92
NM_030887	Mm.10356	U:(C-HI)		NP_569736.1	Jun dimerization protein	244	3.0e+63
NP_112149.1	0	2.07					

NM_009366 NP_033392.1	Mm.20927	U:(C-HI) 2.06, U:(C-D) 2.89, U:(HI-D) 2.64	NP_006013.1	transforming growth factor beta-stimulated protein TSC-22		213	7.0e-54
			BAB46917.1	cerebral protein-2		211	2.0e-53
NM_019992 NP_064376.1	Mm.38392	U:(C-HI) 2.06, U:(C-D) 2.23, U:(HI-D) 2.12	NP_036240.1	BCR downstream signaling 1			
NM_019415 NP_062288.1	Mm.18290 5	U:(C-HI) 2.06	P55017	Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter) (Na-Cl symporter)		1795	0
			G01202	NaCl electroneutral Thiazide-sensitive cotransporter		1792	0
			NP_000330.1	solute carrier family 12 (sodium/chloride transporters), member 3; Solute carrier family 12 (sodium/potassium/chloride transporters),		1792	0
			NP_001037.1	solute carrier family 12 (sodium/potassium/chloride transporters), member 2; Solute carrier family 12 (sodium/potassium/chloride transporters),		1023	0
			NP_000329.1	sodium potassium chloride cotransporter 2; Solute carrier family 12 (sodium/potassium/chloride transporters),		1022	0
			AAH33003.1	lar to solute carrier family 12 (sodium/potassium/chloride transporters), member 2		944	0
			PC4180	thiazide-sensitive sodium-chloride cotransporter - human (fragment)		662	0
			NP_006589.1	solute carrier family 12 (potassium/chloride transporters), member 7; potassium/chloride transporter KCC4			
			AAI32454.1	sodium-potassium-chloride cotransporter		316	1.0e-84
			BAA86490.1	KIAA1176 protein		296	1.0e-78
			AAG43493.1	electroneutral potassium-chloride cotransporter KCC2		271	4.0e-71
			NP_065759.1	solute carrier family 12, (potassium-chloride transporter) member 5		271	4.0e-71

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AK002693	Mm.41325	U:(C-HI)	NP_477513.1	diacylglycerol O-acyltransferase 2 like 1; diacylglycerol acyltransferase 2-like	516	1.0e-145
BAB22288.1		2.04	CAD38961.1	hypothetical protein	311	1.0e-83
			AAH15234.1	Unknown (protein for MGC:17861)	311	1.0e-83
			NP_115953.1	diacylglycerol O-acyltransferase homolog 2; GS1999full	286	4.0e-76
			CAD13492.1	bA351K23.5 (novel protein)	258	1.0e-67
			NP_079374.1	hypothetical protein FLJ22644	241	1.0e-62
			AAD45832.1	similar to predicted proteins AAB54240 (PID:g2132925) and S67138 (PID:g2132925)	208	1.0e-52
AK003722	Mm.89830	U:(C-HI)	NP_008950.1	ubiquitin-conjugating enzyme E2C; ubiquitin carrier protein E2-C	343	1.0e-93
BAB22959.1		2.04	pdb 117K	Ubiquitin-Conjugating Enzyme E2 H10; Chain: A, B; Synonym: Ubiquitin-Conjugating Enzyme Ubch10; Ec: 6.3.2.19;	340	2.0e-92
			CAC36108.1	dJ447F3.2.4 (ubiquitin-conjugating enzyme E2 H10 (isoform 4))	285	8.0e-76
NM_010516	Mm.1231	U:(C-HI)	AAG59863.1	CYR61 protein	650	0
NP_034646.1		2.04	O00622	CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (GIG1 protein)	648	0
			CAA72167.1	CYR61 protein	648	0
			NP_001545.1	cysteine-rich, angiogenic inducer, 61; cysteine-rich heparin-binding protein 61;	645	0
			AAF21597.1	cysteine-rich, angiogenic inducer, 61	486	1.0e-136
			CAC44023.1	tumor RMS cell line RD specific product	330	5.0e-89
			NP_001892.1	bA6918.1 (connective tissue growth factor)	330	5.0e-89
			AAH15028.1	connective tissue growth factor	281	2.0e-74
			NP_002505.1	nephroblastoma overexpressed gene	281	2.0e-74
			AAA75378.1	nov precursor	268	3.0e-70
			NP_003873.1	connective tissue growth factor		
				WNT1 inducible signaling pathway protein 1, isoform 1 precursor; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1; wnt-1 signaling pathway protein 1; connective tissue growth factor related protein WISP-1; Wnt-1 induced secreted protein 1	266	8.0e-70

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				NP_569080.1	WNT1 inducible signaling pathway protein 3, isoform 2; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3	216	7.0e-55
				NP_003871.1	WNT1 inducible signaling pathway protein 3, isoform 1; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3	211	2.0e-53
NM_010354 NP_034484.1	Mm.211109	U:(C-HI) 2.03		NP_000168.1	gelsolin (amyloidosis, Finnish type); Gelsolin	1422	0
				Q9Y6U3	Adseverin (Scinderin)	904	0
				BAC11416.1	unnamed protein product	904	0
				AAK60494.1	scinderin	899	0
				NP_009058.1	villin 1; Villin-1	672	0
				AAD15423.1	similar to mouse adseverin(D5); similar to PID:g2218019	666	0
				BAB67798.1	KIAA1905 protein	666	0
				pdb IDB0	Carboxy-Terminal Half Of Gelsolin (G4-G6) Bound To Actin	643	0
				NP_006567.2	advillin	640	0
				O75366	Advillin (p92)	638	0
				NP_149119.1	scinderin; adseverin; KIAA1905 protein	588	1.0e-167
				AAH17491.1	Similar to gelsolin (amyloidosis, Finnish type)	542	1.0e-153
				BAC11465.1	unnamed protein product	497	1.0e-139
				AAH04134.1	Similar to advillin	464	1.0e-129
				pdb JHWH	Macrophage Capping Protein; Chain: A; Synonym: Actin-Regulatory Protein Cap-G; Engineered	389	1.0e-106
AK002717 XP_134867	Mm.46241	U:(C-HI) 2.02		NP_005692.1	RNA, U transporter 1; snurportin-1; snuportin-1	424	1.0e-169
AK004600 BAB23401.1	Mm.34514	U:(C-HI) 2.02		NP_062455.1	Rho guanine nucleotide exchange factor 3; RhoGEF protein; 59.8 kDA protein	941	0
				BAB14891.1	unnamed protein product	782	0

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				AAH22249.1	Similar to Rho guanine nucleotide exchange factor (GEF) 3	590	1.0e-167
				CAA08974.1	guanine nucleotide-exchange factor	553	1.0e-156
				NP_003015.1	intersectin 1 (SH3 domain protein); intersectin (SH3 domain protein 1A); SH3 domain protein-1A; human intersectin-SH3 domain-containing protein SH3P17	553	1.0e-156
				G01210	guanine nucleotide regulatory protein	500	1.0e-140
5	M62766 AAA37819.1	Mm.2226	U:(C-HI) 2.02	NP_000850.1	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	432	1.0e-120
				pdb 1DQ8	Hmg-CoA Reductase; Chain: A, B, C, D; Fragment: Catalytic Portion; Ec: 1.1.1.34	432	1.0e-120
				AAH33692.1	Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase	432	1.0e-120
10	NM_008299 NP_032325.1	Mm.3075	U:(C-HI) 2.02	NP_005485.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2	263	3.0e-69
				XP_052862.4	similar to DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2	257	2.0e-67
				NP_490647.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a; Heat shock protein J2	252	7.0e-66
				XP_093388.1	similar to DnaJ homolog subfamily B member 8 (mDj6)	197	2.0e-49
15	NM_010877 NP_035007.1	Mm.10729	U:(C-HI) 2.02	AAAM89263.1	p67phox-like protein	826	0
				P19878	Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH oxidase factor 2) (67 kDa neutrophil oxidase factor) (p67-phox)	825	0
				NP_000424.1	neutrophil cytosolic factor 2; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); p67phox	824	0
				AAH01606.1	Similar to neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)	823	0
				pdb 1HH8	Neutrophil Cytosol Factor 2; Chain: A; Fragment: N-Terminal Domain Residues 1 - 213	346	5.0e-94
20				pdb 1E96	Neutrophil Cytosol Factor 2 (Ncf-2) Tpr Domain, Residues 1-203	332	1.0e-89
	NM_019643 NP_062617.1	Mm.18637	U:(C-HI) 2.02	NP_067061.1	TERA protein	402	1.0e-110

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NM_013594 NP_038622.1	Mm.22522	U:(C-HI) 2.01, U:(C-D) 2.15	AAD50371.1	methyl-CpG binding protein 1	779	0
			NP_056671.2	methyl-CpG binding domain protein 1 isoform 1	779	0
			AAD51442.1	methyl-CpG binding protein splice variant 1	773	0
			NP_056670.2	methyl-CpG binding domain protein 1 isoform 2	662	0
			AAD51443.1	methyl-CpG binding protein splice variant 2	657	0
			NP_056723.2	methyl-CpG binding domain protein 1 isoform PCM1	632	1.0e-179
			CAA71735.1	methyl-CpG binding protein	625	1.0e-177
			AAH33242.1	methyl-CpG binding domain protein 1	597	1.0e-169
			NP_056669.1	methyl-CpG binding domain protein 1 isoform 3	596	1.0e-169
			NP_002375.1	methyl-CpG binding domain protein 1 isoform 4	526	1.0e-148
			AAH12487.1	Unknown (protein for MGC:21089)	263	1.0e-68
NM_025566 NP_079842.1	Mm.2312	U:(C-HI) 2	NP_689575.1	hypothetical protein MGC17791	271	1.0e-71
			XP_059012.1	similar to RIKEN cDNA 2600017J23	271	1.0e-71
AK004002 BAB23117.1	Mm.19844	U:(C-HI) 2	CAA36441.1	five-lipoxygenase activating protein (FLAP)	282	3.0e-75
			NP_001620.2	arachidonate 5-lipoxygenase-activating protein; five-lipoxygenase activating protein;	282	3.0e-75
			1603359A	MK-886-binding protein	279	3.0e-74
NM_021366 NP_067341.1	Mm.41170	U:(C-HI) 2	XP_096904.4	lipoxygenase activating protein		
			NP_057079.1	similar to Krueppel-like factor 13 (Transcription factor BTEB3) (Basic transcription element binding protein 3) (BTE-binding protein 3) (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Transcription factor NSLP1) (Novel Sp1-like zinc fi	306	3.0e-82
				Kruppel-like factor 13; transcription factor NSLP1; novel Sp1 like zinc finger transcription factor; RANTES factor of late activated T lymphocytes-1; basic transcription element binding protein 3	305	8.0e-82

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NM_025566		U:(C-HI)	NP_689575.1			271	1.0e-71
NP_079842.1	Mm.2312	+2	XP_059012.1	hypothetical protein MGC17791 similar to RIKEN cDNA 2600017J23		271	1.0e-71
NM_023873							
NP_076362.1	Mm.18879	U:(C-D)+ 1.9	AAH30598	p10-binding protein	822	822	0
			NP_077817	p10-binding protein	815	815	0
			BAB14403	unnamed protein product	812	812	0
			AAG35791	p10-binding protein BITE splice variant	763	763	0
			AAH16050	Similar to p10-binding protein	311	311	4.0e-84
NM_009252	Mm.22650	U:(C-D)+ 1.77	CAA48671.1	alpha1-antichymotrypsin	497	497	1.1e-138
NP_033278.1			XP_028322.1	similar to Alpha-1-antichymotrypsin precursor (ACT)	494	494	1.0e-138
			AAH34554.1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	493	493	1.0e-138
			ITHUC	alpha-1-antichymotrypsin precursor - human	482	482	1.0e-135
			AAD08810.1	alpha-1-antichymotrypsin precursor	481	481	1.0e-134
			AAA51560.1	alpha-1-antichymotrypsin precursor	471	471	1.0e-131
			pdj1QMN	alpha - 1-Antichymotrypsin	461	461	1.0e-128
			I313184C	chymotrypsin inhibitor	439	439	1.0e-122
			pdj2ACH	alpha1 Antichymotrypsin	438	438	1.0e-121
			NP_001076.1	alpha-1-antichymotrypsin, precursor; alpha-1-antichymotrypsin; antichymotrypsin	437	437	1.0e-121
			pdj3CAA	Cleaved Antichymotrypsin A347R	426	426	1.0e-118
			pdj1AS4	Cleaved Antichymotrypsin A349R	426	426	1.0e-118
			pdj4CAA	Cleaved Antichymotrypsin T345R	426	426	1.0e-118
			NP_006206.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4; protease inhibitor 4 (kallistatin)	310	310	6.0e-83
			P29622	Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4)	310	310	6.0e-83

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			NP_000615.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)	307	3.0e-82
			T12502	hypothetical protein DKFZp434P131.1	307	3.0e-82
			AAB60386.1	protein C inhibitor	307	4.0e-82
			AAA35688.1	plasma serine proteinase inhibitor precursor	307	4.0e-82
			pdj1ATU	Uncleaved alpha-1-Antitrypsin	305	2.0e-81
			pdj1KCT	Alpha 1-Antitrypsin	305	2.0e-81
			NP_000286.2	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	305	2.0e-81
			I313184B	alpha1 antitrypsin	304	3.0e-81
			AAA51547.1	alpha-1-antitrypsin precursor	304	3.0e-81
			AAH15642.1	Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	304	3.0e-81
			AAA51546.1	alpha-1-antitrypsin	303	5.0e-81
			AAB26244.2	acrosomal serine protease inhibitor	303	6.0e-81
			P01009	Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (PRO0684/PRO2209)	303	6.0e-81
NM_011905	U:(C-D)+					
NP_036035.1	Mm.87596	1.6	NP_003255	toll-like receptor 2; toll/interleukin 1 receptor-like 4	1050	0
			AAC34133	Toll-like receptor 2	1048	0
			AAM23001	Toll-like receptor 2	705	0
			NP_003254	toll-like receptor 1; Toll/interleukin-1 receptor-like	322	2.0e-87
			BAA02801	KIAA0012	320	7.0e-87
			T08664	Toll protein-like receptor DKFZp547I0610.1 - human	318	2.0e-86
			NP_112218	toll-like receptor 10 precursor	318	2.0e-86
			NP_006059	toll-like receptor 6	312	1.0e-84
			Q9Y2C9	Toll-like receptor 6 precursor	310	5.0e-84
			I077A	Chain A, Crystal Structure Of The C713s Mutant Of The Tir Domain Of Human Tir2	281	4.0e-75

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			1FYXA	Chain A, Crystal Structure Of P681h Mutant Of Tir Domain Of Human Tlr2.	266	9.0e-91
			1FYWA	Chain A, Crystal Structure Of The Tir Domain Of Human Tlr2.	264	4.0e-70
AK017185		U:(C-D)				
BAB30625.1	Mm.26935	+2.9	Q15771	Ras-related protein Rab-30	401	1.0e-110
NM_011704	Mm.27154	U	NP_004657.1	vanin 1 precursor; Vannin 1; pantetheinase		
NP_035834.1		(C-HI)+4 .37, U (C-D) 3.14, U (HI-D) 2.37			795	0
			AAF21453.1	Tiff66	793	0
			CAB40075.1	dJ55C23.1 (vanin 1)	793	0
			NP_060869.1	vanin 3 isoform 1 precursor; VNN3 protein; pantetheinase	657	0
			CAB40076.1	dJ55C23.2 (vanin 2)	639	0
			NP_004656.2	vanin 2, isoform 1 precursor; Vannin 2; pantetheinase	638	0
			CAA10569.1	VNN2 protein	635	0
			NP_511043.1	vanin 2, isoform 2; Vannin 2; pantetheinase	597	1.0e-169
			P43251	Biotinidase precursor	382	1.0e-105
			NP_000051.1	biotinidase precursor	382	1.0e-105
			CAC33872.1	dJ55C23.5.1 (vanin 3, isoform 1)	342	1.0e-92

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NM_007468 NP_031494.1	Mm.4533	U (C-HI)+2 .98, U (C-D) 2.42, U (HI-D) 2.16	P06727	Apolipoprotein A-IV precursor (Apo-AIV)		432	1.0e-120
			CAA31955.1	apolipoprotein A-IV precursor		431	1.0e-119
			NP_000473.1	apolipoprotein A-IV precursor		428	1.0e-119
			LPHUA4	apolipoprotein A-IV precursor [validated]		426	1.0e-118
			AA51748.1	apolipoprotein A-IV precursor		422	1.0e-117
			AAB59516.1	apolipoprotein A-IV		277	2.0e-73
NM_016974 NP_058670.1	Mm.3459	U (C-HI) 2.79, U (C-D) 4.24, U (HI-D) 2.47	Q10586	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)		399	1.0e-110
			NP_001343.1	D site of albumin promoter (albumin D-box) binding protein; D site of albumin promoter binding protein		399	1.0e-110
			BAA05833.1	TAXREB302		299	9.0e-80
			NP_002117.1	hepatic leukemia factor		203	5.0e-51
			Q10587	Thyrotroph embryonic factor		201	2.0e-50
			B55558	thyrotroph embryonic factor - human		201	2.0e-50
			CAB62497.1	dJ979N1.5 (thyrotrophic embryonic factor (ortholog of chicken vitellogenin gene-binding protein VBP beta/beta isoform) (isoform 2))		201	2.0e-50
			NP_003207.1	thyrotrophic embryonic factor; Thyrotroph embryonic factor		101	3.0e-20

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NM_019634	Mm.18590	U:(HI-D)	NP_004606.2	transmembrane 4 superfamily member 2; membrane component, x chromosome, surface marker 1; T-cell acute lymphoblastic leukemia associated antigen 1;	497	1.0e-139
NP_062608.1		2.86		transmembrane protein A15; tetraspanin protein; cell surface glycoprotein A15; CD231 antigen; transmembrane 4 superfamily 2b		
			CAB65594.1	tetraspanin protein.	496	1.0e-139
			I39368	T-cell acute lymphoblastic leukemia associated antigen 1 - human	495	1.0e-139
			AAH18036.1	Unknown (protein for MGC:26217)	494	1.0e-138
			AAF44123.1	TALLA-1	450	1.0e-125
			NP_003261.1	transmembrane 4 superfamily member 6; tetraspan TM4SF; A15 homolog; tetraspanin TM4-D; tetraspanin 6	295	1.0e-78
NM_008597	Mm.19345	U:(HI-D)	NP_000891.1	matrix Gla protein	167	7.0e-41
NP_032623.1	9	2.36				
NM_009234	Mm.6238	U:(HI-D)	NP_003099.1	SRY (sex determining region Y)-box 11; SRY (sex-determining region Y)-box 11	415	1.0e-115
NP_033260.1		2.36				
NM_009964	Mm.178	U:(HI-D)	O43416	HEAT-SHOCK 20 KD LIKE-PROTEIN	337	1.0e-91
NP_034094.1		2.06				
			NP_001876.1	crystallin, alpha B; crystallin, alpha-2; Rosenthal fiber component; heat-shock 20 kD like-protein	336	3.0e-91
NM_013565	Mm.57035	U:(HI-D)	NP_002195.1	integrin alpha 3 isoform a precursor	1778	0
NP_038593.1		2.05			1741	0
			BAA00845.1	VLA-3 alpha subunit		
			P26006	Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c)	1723	0
			NP_005492.1	integrin alpha 3 isoform b, precursor	1721	0
			CAA42099.1	integrin alpha6 subunit	587	1.0e-166
			NP_000201.1	integrin alpha chain, alpha 6	582	1.0e-164
			AAD48469.1	integrin alpha 6	582	1.0e-164
			B36429	integrin alpha-6 chain precursor, splice form A [validated]	578	1.0e-163
			CAB41534.1	integrin alpha 7 chain	576	1.0e-163
			NP_002197.1	integrin alpha 7 precursor	575	1.0e-162
			AAC18968.1	integrin alpha 7	573	1.0e-162

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				Q13683	Integrin alpha-7 precursor	561	1.0e-158
				A41543	Integrin alpha-6 chain precursor, splice form B	560	1.0e-158
				P23229	Integrin alpha-6 precursor (VLA-6) (CD49f)	557	1.0e-157
NM_013805	Mm.22768	U:(H1-D)		AAH19290.1	Unknown (protein for IMAGE:2822745)	320	4.0e-86
NP_038833.1		2.04		NP_003268.1	transmembrane protein claudin 5; androgen withdrawal and apoptosis induced protein RVP1 (rat)-like; Claudin-5 (transmembrane protein deleted in velocardiofacial syndrome)	315	1.0e-84
AK014697	Mm.15956	U:(H1-D)		NP_110415.1	DC-specific transmembrane protein	525	1.0e-147
BAB29508.1	3	2.01					

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Master Table 1: Subtable 1C: Mixed Genes/Proteins

Mouse Gene Protein	Unigene	Behavior	Human Protein	Human Protein Name	Score	E-Value
NM_016875	Mm.29286	U:(H-I-D)	NP_057066.1	germ cell specific Y-box binding protein; contrin		
NP_058571.1		2.73 F:(C-D)				
		-4.72			285	1.00e-75
			AAH33800.1	germ cell specific Y-box binding protein	285	1.00e-75
AF001293		U:(H-I-D)	XP_012694.8	similar to zinc finger protein, subfamily 1A, 3 (Aiolos)		
AAB58795.1	Mm.37444	2.59 F:(C-D)				
		-3.71			920	0
			NP_036613.1	zinc finger protein, subfamily 1A, 3 (Aiolos)	911	0
			CAC80429.1	Aiolos isoform four	822	0
			CAC80427.1	AIOLOS isoform two	753	0
			CAC80428.1	AIOLOS isoform three	735	0
			CAC80431.1	AIOLOS isoform six	548	1.00e-145
			CAC80430.1	AIOLOS isoform five	516	1.00e-145
			NP_006051.1	zinc finger protein, subfamily 1A, 1 (Ikaros); Ikaros (zinc finger protein)	506	1.00e-142
			AAB50683.1	hlk1	493	1.00e-138
			NP_057344.1	zinc finger protein, subfamily 1A, 2 (Helios); zinc finger DNA binding protein Helios	466	1.00e-130
			AAH18349.1	Unknown (protein for MGC:17055)	448	1.00e-124
			AAH28936.1	Similar to zinc finger protein, subfamily 1A, 2 (Helios)	417	1.00e-115
			BAB47411.1	KIAA1782 protein	406	1.00e-112
			NP_071910.1	zinc finger protein, subfamily 1A, 4 (Eos); zinc finger transcription factor Eos	403	1.00e-111

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NM_009895 NP_034025.1	Mm.4592	U:(HI-D) 2.45 F:(C-D) -2.25	NP_659508.1	cytokine-inducible SH2-containing protein isoform 2; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling	469	1.00e-131
			AAF97410.1	cytokine-inducible inhibitor of signalling type 1b	456	1.00e-127
			NP_037456.4	cytokine-inducible SH2-containing protein isoform 1; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling	456	1.00e-127
NM_018830 NP_061300.1	Mm.10490 0	U:(HI-D) 2.42 F:(C-D) -2.62	NP_063946.1	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2; N-acylsphingosine amidohydrolase 2; mitochondrial ceramidase; N-acylsphingosine amidohydrolase (acid ceramidase) 2	1219	0
AF398969 AAK97491.1	Mm.20076 6	U:(HI-D) 2.35 F:(C-D) -2.5	NP_077000.1	ankyrin repeat and SOCS box-containing 8	552	1.00e-156
NM_016970 NP_058666.1	Mm.20434	U:(HI-D) 2.13 F:(C-D) -2.74	AAC32200.1	ITIM-containing receptor MAFA-L	223	6.00e-57
			NP_005801.2	killer cell lectin-like receptor subfamily G, member 1; mast cell function-associated antigen (ITIM-containing)	221	2.00e-56
			AAC34731.1	mast cell function-associated antigen	215	1.00e-54
NM_009344 NP_033370.1	Mm.3117	U:(HI-D) 2.1 F:(C-D) -3.91	NP_031376.1	pleckstrin homology-like domain, family A, member 1; PQ-rich protein	379	1.00e-104
			AAH18929.1	Similar to T-cell death associated gene	235	1.00e-60

NM_009255 NP_033281.1	Mm.3093	U:(HI-D) 2.01 F:(C-D) -2.61	XP_059422.1	similar to tropomyosin, fibroblast - human	691	0
			P07093	Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease inhibitor 7)	684	0
			A26061	glia-derived neurite promoting factor precursor	682	0
			pdj IDB2	Plasminogen Activator Inhibitor-1	310	4.00e-83
			CAA28444.1	plasminogen activator inhibitor	310	4.00e-83
			pdj ILJ5	Plasminogen Activator Inhibitor-1; Chain: A; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai	310	4.00e-83
			NP_000593.1	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1; plasminogen activator inhibitor, type I	310	4.00e-83
			AAA60008.1	prebeta-migrating plasminogen activator inhibitor	310	4.00e-83
			AAA60009.1	plasminogen activator inhibitor 1	308	1.00e-82
			pdj 9PAI	Cleaved Substrate Variant Of Plasminogen Activator Inhibitor-1	308	1.00e-82
			pdj LA7C	Human Plasminogen Activator Inhibitor Type-1 In Complex With A Pentapeptide	308	2.00e-82
			pdj IB3K	Plasminogen Activator Inhibitor-1	307	3.00e-82
			pdj IDVM	Active Form Of Human Pai-1	305	2.00e-81
			CAA31208.1	PAI precursor polypeptide	305	2.00e-81
			NP_005016.1	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1; protease inhibitor 12 (neuroserpin)	243	7.00e-63
			AAH18043.1	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1	240	5.00e-62
			NP_006208.1	protease inhibitor 14; pancpin	216	1.00e-55
NM_020013 NP_064397.1	Mm.14373 6	U:(C-HI) 6.00, U:(C-D) 5.03, F:(HI-D) -3.06	AAH18404.1	fibroblast growth factor 21		
			NP_061986.1	fibroblast growth factor 21 precursor	301	3.00e-81
					298	5.00e-80

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X82786 CAA58026.1	Mm.4078	U:(C-HI) 4.07, F:(HI-D) -4.25	NP_002408.2	antigen identified by monoclonal antibody Ki-67; Proliferation-related Ki-67 antigen	1711	0
			CAA46520.1	antigen of the monoclonal antibody Ki-67	1315	0
			B48666	cell proliferation antigen Ki-67, short form - human	1276	0
NM_010000 NP_034130.1	Mm.876	U:(C-HI) 34.21, U:(C-D) 8.32, F:(HI-D) -3.81	NP_000758.1	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6		0
			AAF13602.1	cytochrome P450-2B6	665	0
			NP_000757.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13	499	1.00e-140
			Q16696	Cytochrome P450-2A13 (CYP1A13)	494	1.00e-138
			O4HUA6	coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 - human	489	1.00e-137
			CAA32117.1	P-450 IIA3 protein (1 is 3rd base in codon)	489	1.00e-137
			NP_000753.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	487	1.00e-136
			CAA32097.1	cytochrome P-450IIA (AA 1 - 489)	486	1.00e-136
			1609083A	cytochrome P450IIA	486	1.00e-136
			P11509	Cytochrome P450 2A6 (CYP1A6) (Coumarin 7-hydroxylase) (IIA3) (CYP2A3) (P450(I))	486	1.00e-136
			AAF13600.1	cytochrome P450-2A6	485	1.00e-136
			C34271	cytochrome P450 2A4 - human.	485	1.00e-135
			P20853	Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)	484	1.00e-135
			NP_000755.2	cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 1	483	1.00e-135
			I38965	cytochrome P450 - human	480	1.00e-134

	AAA52143.1	cytochrome P450-11B	478	1.00e-134
	I38967	cytochrome P450 - human	471	1.00e-131
	AAH20596.1	Unknown (protein for MGC:22146)	462	1.00e-129
	P10632	Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12MP-20) (P450 11C2) (S-mephenytoin 4-hydroxylase)	462	1.00e-129
	NP_000765.2	cytochrome P450, subfamily 11F, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily 11F, polypeptide 1	461	1.00e-128
	AAA52161.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	461	1.00e-128
	NP_000761.2	cytochrome P450, subfamily 11C, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	459	1.00e-128
	NP_000763.1	cytochrome P450, subfamily 11C (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily 11C (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	458	1.00e-127
	AAA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	458	1.00e-127
	S66382	cytochrome P450 2C8 - human	458	1.00e-127
	AAB35292.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]	458	1.00e-127
	P33260	Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	456	1.00e-127
	AAL69652.1	cytochrome P450 2F1	455	1.00e-126
	BAA00123.1	cytochrome P-450	449	1.00e-125
	NP_000762.2	cytochrome P450, subfamily 11C, polypeptide 9; cytochrome P450, subfamily 11C (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	449	1.00e-125
	AAB23864.2	cytochrome P-450	449	1.00e-125
	P11713	Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	445	1.00e-123
	AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	445	1.00e-123

				NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	444	1.00e-123
NM_009689 NP_033819.1	Mm.8552	U:(C-HI) 3.67, F:(HI-D) -3.5		NP_001159.1	baculoviral IAP repeat-containing protein 5; apoptosis inhibitor 4; survivin		
				pdb 1F3H	Survivin; Chain: A, B; Synonym: Apoptosis Inhibitor 4	258	6.00e-68
				BAA93676.1	survivin-beta	258	1.00e-67
NM_010634 NP_034764.1	Mm.741	U:(C-HI) 3.17, F:(HI-D) -5.62		NP_001435.1	fatty acid binding protein 5 (psoriasis-associated); E-FABP	245	5.00e-64
						220	2.00e-56
NM_007659 NP_031685.1	Mm.4761	U:(C-HI) 3.00, F:(HI-D) -2.87		NP_001777.1	cell division cycle 2 protein, isoform 1; cell division control protein 2 homolog; cyclin-dependent kinase 1; p34 protein kinase; cell cycle controller CDC2	577	1.00e-163
				NP_001249.1	cyclin-dependent kinase 3	393	1.00e-108
				CAA43807.1	cell division kinase. CDC2 homolog	390	1.00e-107
				NP_001789.2	cyclin-dependent kinase 2, isoform 1; cdc2-related protein kinase; cell division kinase 2; p33 protein kinase	389	1.00e-107
				pdb 1E1X	Cyclin-Dependent Protein Kinase 2; Chain: A; Synonym: Cdk2; Ec: 2.7.1.37	389	1.00e-107
				pdb 1E9H	Cyclin-Dependent Kinase 2, Cdk2; Ec: 2.7.1.37	387	1.00e-106
				pdb 1GY3	Pcdk2/Cyclin A In Complex With Mgapd, Nitrate and Peptide Substrate	387	1.00e-106
				CAA43985.1	cdk2	387	1.00e-106
				pdb 1JST	Cyclin-Dependent Kinase-2; Chain: A, C; Synonym: Cdk2; Ec: 2.7.1.-	387	1.00e-106
				pdb 1GII	Cell Division Protein Kinase 2; Chain: A; Synonym: Cyclin Dependent Kinase 2; Ec: 2.7.1.37	382	1.00e-105
				AAH33005.1	PCTAIRE protein kinase 2	327	2.00e-88

			S23384	protein kinase (EC 2.7.1.37) cdc2-related PCTAIRE-2 - human	326	3.00e-88
			NP_002586.1	PCTAIRE protein kinase 2; serine/threonine-protein kinase PCTAIRE-2; protein kinase cdc2-related PCTAIRE-2	324	2.00e-87
			pdj1H4L	Cdk5-P25(Nck5A) Complex - Protein Kinase II Catalytic Subunit, Cdk5 - Cdk5 Activator 1, Cyclin-Dependent Kinase 5 Regulatory Subunit 1, Protein Kinase II 23 Kda Subunit, TpkII Regulatory Subunit, P23, P25, P35	320	2.00e-86
			NP_004926.1	cyclin-dependent kinase 5	320	2.00e-86
			JE0374	cyclin-dependent kinase 5 (EC 2.7.-.-) - human	320	2.00e-86
NM_007822 NP_031848.1	Mm.7459	U:(C-HI) 24.5, F:(C-D) -5.06, F:(HI-D) -7.06	NP_000769.1	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase	780	0
			Q02928	Cytochrome P450 4A11 precursor (CYP1A11) (Fatty acid omega-hydroxylase) (P-450 HK omega) (Lauric acid omega-hydroxylase) (CYP4A11) (P450-HL-omega)	777	0
			I65981	fatty acid omega-hydroxylase (EC 1.14.15.-) cytochrome P450 4A11 - human	765	0
			BAA02864.1	fatty acid omega-hydroxylase	761	0
			AAF76722.1	fatty acid omega-hydroxylase CYP4A11	746	0
			CAB72105.1	dJ18D14.4 (cytochrome P450, subfamily IVA, polypeptide 11)	736	0
			O4HUB1	cytochrome P450 4B1 - human	499	1.00e-139
			AAL57720.1	cytochrome P450	499	1.00e-139
			AAM09532.1	cytochrome P450	499	1.00e-139
			NP_000770.1	cytochrome P450, subfamily IVB, polypeptide 1; cytochrome P450, subfamily IVB, member 1; microsomal monooxygenase	497	1.00e-139
			AAL57721.1	cytochrome P450	497	1.00e-139
			AAH17758.1	Unknown (protein for MGC:22150)	495	1.00e-138
			AAH28102.1	Unknown (protein for MGC:40051)	489	1.00e-137
			BAC03751.1	unnamed protein product	448	1.00e-124
			BAC04868.1	unnamed protein product	402	1.00e-110

				BAA75823.1	Leukotriene B4 omega-hydroxylase	398	1.00e-109
				NP_001073.3	tochrome P450, subfamily IVF, polypeptide 2; leukotriene B4 omega-hydroxylase; leukotriene-B4 20-monooxygenase	398	1.00e-109
				NP_000887.1	cytochrome P450, subfamily IVF, polypeptide 3; leukotriene B4 omega hydroxylase; leukotriene-B4 20-monooxygenase; cytochrome P450-LTB-omega	394	1.00e-108
				AAC50052.2	cytochrome P450 4F2	393	1.00e-108
				AAC08589.1	cytochrome P-450	390	1.00e-107
				Q9HB16	Cytochrome P450 4F11 (CYP1VF11)	387	1.00e-106
				NP_067010.1	cytochrome P450, subfamily IVF, polypeptide 11	387	1.00e-106
				Q9HCS2	Cytochrome P450 4F12 (CYP1VF12)	384	1.00e-105
				NP_076433.1	cytochrome P450 isoform 4F12	384	1.00e-105
				AAH35350.1	similar to cytochrome P450	384	1.00e-105
				AAC11543.1	F22329_1	381	1.00e-104
				NP_009184.1	cytochrome P450, subfamily IVF, polypeptide 8; microsomal monooxygenase; flavoprotein-linked monooxygenase	380	1.00e-104
				CAD38795.1	hypothetical protein	347	6.00e-94
				XP_065069.2	similar to CYTOCHROME P450 4F6 (CYP1VF6)	337	6.00e-91
				XP_029070.2	similar to Cytochrome P450 4F12 (CYP1VF12)	323	9.00e-87
				AAH22851.1	Similar to cytochrome P450, subfamily IVA, polypeptide 11	287	6.00e-76
				XP_065068.1	similar to Cytochrome P450 4F12 (CYP1VF12)	278	2.00e-73
				BAC05026.1	unnamed protein product	278	2.00e-73
				BAA02145.1	cytochrome P-450LTBV	270	6.00e-71
				CAA50586.1	cytochrome P450	263	1.00e-68
				AAL57719.1	truncated cytochrome P450	237	5.00e-61
NM_010286	Mm.22216	U:(C-HI)	Q99576		Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R)		
NP_034416.1		2.83, F:(HI-D)				196	8.00e-49
		-2.17				188	2.00e-46
				TI14749	hypothetical protein DKFZp566A093.1 - human		

NM_008362 NP_032388.1	Mm.896	U:(C-HI) 2.59, F:(HI-D) -2.22	NP_000868.1	Interleukin 1 receptor, type I	823	0
			pdj11IRA	Interleukin-1 Receptor Antagonist; Chain: X; Synonym: IL1Ra	451	1.00e-125
			pdj11ITB	Type-1 Interleukin-1 Receptor Complexed With Interleukin-1 Beta	448	1.00e-124
			pdj11G0Y	IL-1 Receptor Type 1 Complexed With Antagonist Peptide Af10847	445	1.00e-123
			XP_002685.3	similar to IL-1Rrp2	562	2.00e-96
			AAg21368.1	IL-1Rrp2	356	2.00e-96
			NP_003845.1	interleukin 1 receptor-like 2	354	7.00e-96
			NP_057316.2	interleukin 1 receptor-like 1; interleukin 1 receptor 1; ST2V protein	208	5.00e-52
			NP_059112.1	interleukin 1 receptor accessory protein-like 2	206	3.00e-51
			AAF59412.1	X-linked interleukin-1 receptor accessory protein-like 2	206	3.00e-51
NM_019977 NP_064361.1	Mm.15820 0	U:(C-HI) 2.51 F:(C-D) -2.15	AAF25204.1	unknown		
			NP_060054.2	aldehyde reductase (aldose reductase) like 6; similar to mouse aldehyde reductase 6 (renal); myo-inositol oxygenase; kidney-specific protein 32	540	1.00e-152
			AAK00766.1	kidney-specific protein 32	535	1.00e-151
NM_010544 NP_034674.1	Mm.2543	U:(C-HI) 2.45, F:(HI-D) -2.47	Q14623	Indian hedgehog protein precursor (IHH) (HHG-2)	528	1.00e-149
			AAA62178.1	Indian hedgehog protein	725	0
			XP_050846.2	similar to Indian hedgehog protein precursor (IHH) (HHG-2)	612	1.00e-174
			2117287B	Indian hedgehog gene	578	1.00e-163
			NP_000184.1	sonic hedgehog preproprotein	553	1.00e-156
			NP_066382.1	desert hedgehog preproprotein	451	1.00e-125
			2117287A	Sonic hedgehog gene	428	1.00e-118
					420	1.00e-116

				AAB67604.1	Sonic Hedgehog; associated with holoprosencephaly in humans and segment polarity defects in Drosophila	296	8.00e-79
NM_011819 NP_035949.1	Mm.31325 U:(C-HI) 2.39, U:(C-D) 2.00, F:(HI-D) -2.52	JC5697			placental transforming growth factor-beta homolog - human		
		AAC39537.1			prepro placental TGF-beta	284	2.00e-75
		XP_038098.1			similar to Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)...	281	1.00e-74
		AAC24456.1			prostate differentiation factor	281	1.00e-74
		Q99988			Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)	281	2.00e-74
		NP_004855.1			ate differentiation factor; PTGF-beta	280	5.00e-74
NM_019641 NP_062615.1	Mm.28479 U:(C-HI) 2.29, F:(HI-D) -2.08	NP_005554.1			stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; stathmin; leukemia-associated phosphoprotein p18		
		AAH14353.1			Similar to stathmin 1/oncoprotein 18	286	6.00e-77
NM_010121 NP_034251.1	Mm.23375 U:(C-HI) 2.15, F:(HI-D) -2.19	Q9NZJ5			Eukaryotic translation initiation factor 2-alpha kinase 3 precursor (PRKR-like endoplasmic reticulum kinase) (Pancreatic eIF2-alpha kinase) (HsPEK)	285	2.00e-76
		NP_004827.2			eukaryotic translation initiation factor 2-alpha kinase 3; eukaryotic translation initiation factor 2 alpha kinase 3	1759	0
						1757	0

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NM_011579 NP_035709.1	Mm.15793	U:(C-HI) 2.13 F:(C-D) -2.1	NP_062558.1	hypothetical protein R30953_1	233	4.00e-60
NM_011318 NP_035448.1	Mm.2165	U:(C-HI) 2.03, F:(HI-D) -2.37	AAA60302.1	pre-serum amyloid P component		
			NP_001630.1	serum amyloid P component precursor; amyloid P component, serum; pentaxin-related; 9.5S alpha-1-glycoprotein	316	3.00e-85
			pdj1SAC	Serum Amyloid P Component (Sap)	296	2.00e-79
			XP_049673.1	similar to C-reactive protein precursor	233	2.00e-60
			pdj1LJ7	C-Reactive Protein; Chain: A, B, C, D, E, F, G, H, I, J	223	2.00e-57
			NP_000558.1	C-reactive protein, pentraxin-related; C-reactive protein	214	2.00e-54
NM_016847 NP_058543.1	Mm.4351	U:(C-HI) 2.02, F:(HI-D) -2.03	NP_000697.1	arginine vasopressin receptor 1A; V1a vasopressin receptor; vascular/hepatic-type arginine vasopressin receptor; antidiuretic hormone receptor 1A	701	0
			NP_000698.1	arginine vasopressin receptor 1B; arginine vasopressin receptor 3; antidiuretic hormone receptor 1B; vasopressin V1B receptor; pituitary vasopressin receptor 3	364	4.00e-99
			NP_000907.1	oxytocin receptor	355	2.00e-96
			1808301A	oxytocin receptor	355	2.00e-96
			CAA56562.1	oxytocin receptor	299	1.00e-79
			NP_000045.1	arginine vasopressin receptor 2	244	5.00e-63
			1913493A	vasopressin receptor:ISO TYPE=V2	241	3.00e-62
			AAB87678.1	vasopressin receptor type 2	216	1.00e-54

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C76314 NP_690023.1	Mm.28270	U:(C-D) 2.97 F:(C-D) -2.87	BAA24862.2	KIAA0432		236	2.00e-99
			NP_001244.1	CDC5-like; CDC5 (cell division cycle 5, S. pombe, homolog)-like; Cell division cycle 5, S. pombe, homolog-like; Cdc5-related protein		236	2.00e-99
			CAC08557.1	dJ319D22.1 (CDC5-like protein)		236	6.00e-95
NM_011128 NP_035258.1	Mm.1230	U:(C-D) 2.35, U:(HI-D) 2.73 F:(C-D) -2.85	NP_005387.1	pancreatic lipase-related protein 2			
			NP_000927.1	pancreatic lipase		748	0
			pdb 1LPB	Lipase (E.C. 3.1.1.3) Complexed With Colipase and Inhibited By Undecane Phosphonate Methyl Ester		668	0
			1604419A	lipase		646	0
			NP_006220.1	pancreatic lipase-related protein 1		631	1.00e-180
			AAH25784.1	pancreatic lipase-related protein 1		630	1.00e-179
			CAA22264.1	dA149D17.1 (PLRP2 (PNLIPRP2, Pancreatic Lipase Related Protein 2 Precursor, EC 3.1.1.3) LIKE protein)			
NM_008239 NP_032265.2	Mm.44235	U:(C-D) 2.23, U:(HI-D) 2.15 F:(C-D) -2.79	NP_150285.1	winged helix/forkhead transcription factor		217	3.00e-55
			AAK00639.1	HNF-3/forkhead-like protein 1		344	
						342	

NM_020277 NP_064673.1	Mm.14374 7	U:(C-D) 2.05, U:(HI-D) 2.32 F:(C-D) -4.69	NP_055370.1	transient receptor potential cation channel, subfamily M, member 5; MLSN1 and TRP-related; MLSN1- and TRP-related	1875	0
			CAB66342.1	LTRPC5 protein	1875	0
			NP_060106.2	transient receptor potential cation channel, subfamily M, member 4	833	0
			AAL02142.1	TRP-related cation influx channel	728	0
			BAA90907.1	unnamed protein product	726	0
			BAA95563.1	transient receptor potential-related channel 7, a novel putative Ca2+ channel protein	696	0
			NP_003298.1	transient receptor potential cation channel, subfamily M, member 2; transient receptor potential-related channel 7, a novel putative Ca2+ channel protein; transient receptor potential channel 7	696	0
			CAD01139.1	putative TRP cation channel	688	0
			BAB86335.1	LTRPC6	510	1.00e-143
			NP_076985.3	transient receptor potential cation channel, subfamily M, member 8	510	1.00e-143
			NP_060132.3	transient receptor potential cation channel, subfamily M, member 6	398	1.00e-109
			AAK19738.2	channel-kinase 1	317	7.00e-85
			XP_030709.6	similar to LTRPC7	317	7.00e-85
			BAB15429.1	unnamed protein product	295	3.00e-78
			AAC80000.1	melastatin 1	270	1.00e-70
			NP_002411.2	transient receptor potential cation channel, subfamily M, member 1; melastatin 1 [270	1.00e-70
NM_019922 NP_064306.1	Mm.20904	U:(C-D) 2.05 F:(C-D) -2.29	AAH08745.1	cartilage associated protein	666	0
			NP_006362.1	cartilage associated protein; cartilage-associated protein	666	0
			BAC03743.1	unnamed protein product	633	1.00e-180
			CAC16786.1	nucleolar protein No55	403	1.00e-111

AF047725 AAD13720.1	Mm.42100	F:(H-I-D) -2.06 U:(C-D) 2.35	NP_006446.1 NP_000763.1	nucleolar autoantigen (55kD) similar to rat synaptonemal complex cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase	402	1.00e-111
			P33260	Cytochrome P450 2C18 (CYP1IC18) (P450-6B/29C)	704	0
			NP_000760.1	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	683	0
			P10632	Cytochrome P450 2C8 (CYP1IC8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)	681	0
			AAH20596.1	Unknown (protein for MGC:22146)	680	0
			NP_000762.2	cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase	679	0
			AAB23864.2	cytochrome P-450 [Homo sapiens]	679	0
			AAA52161.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	679	0
			BAA00123.1	cytochrome P-450 [Homo sapiens]	679	0
			NP_000761.2	cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1	678	0
			S66382	cytochrome P450 2C8 - human.	677	0
			AAB35292.1	cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human; kidney, Peptide Partial, 485 aa]	677	0
			AAA52160.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	677	0
			F38462	S-mephenytoin 4'-hydroxylase (EC 1.14.14.-) cytochrome P450 2C19	676	0
			P11713	Cytochrome P450 2C10 (CYP1IC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)	674	0
			AAA52157.1	cytochrome P-450 S-mephenytoin 4-hydroxylase	674	0
			1506290A	cytochrome P450	674	0

AK007530			IS2418	cytochrome P450 - human	640	0
BAB25091.1	Mm.46315	F:(C-HI) -7.8, F:(C-D) -2.61, U:(HI-D) 2.99	NP_003951.2	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene		
			NP_057431.1	putative N-acetyltransferase Camello 2	190	2.00e-48
			BAA71643.1	GLA	189	4.00e-48
			AAH12626.1	kidney- and liver-specific gene	189	4.00e-48
			T44342	hypothetical protein TSC501 [imported]	188	1.00e-47
NM_007825	Mm.4781	F:(C-HI) -6.41, U:(HI-D) 5.83	AAC95426.1	oxysterol 7alpha-hydroxylase	188	1.00e-47
NP_031851.1						
			NP_004811.1	cytochrome P450, subfamily VIIIB, polypeptide 1; oxysterol 7alpha-hydroxylase	640	0
			P22680	Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase)	640	0
NM_015763	Mm.28548	F:(C-HI) -3.7, U:(C-D) 3.14	Q14693	Lipin 1	313	5.00e-85
NP_056578.1						
			NP_663731.1	lipin 1	1493	0
			AAH30537.1	Similar to lipin 1	1488	0
			XP_041136.4	similar to Hypothetical protein KIAA0188	1487	0
			NP_055461.1	lipin 2	1476	0
					790	0

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X71479 CAA50585.1	F:(C-HI) -3.57, F:(C-D) -2.54, U:(HI-D) 2.82	CAA50586.1	cytochrome P450		268	2.00e-72
		NP_000769.1	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase		267	4.00e-72
		I65981	fatty acid omega-hydroxylase (EC 1.14.15.-) cytochrome P450 4A11 - human		267	4.00e-72
		Q02928	Cytochrome P450 4A11 precursor (CYP1A11) (Fatty acid omega-hydroxylase) (P-450 HK omega) (Lauric acid omega-hydroxylase) (CYP4A11) (P450-HL-omega)		265	2.00e-71
		BAA02864.1	fatty acid omega-hydroxylase		265	2.00e-71
		AAF76722.1	fatty acid omega-hydroxylase CYP4A11		261	1.00e-70
		CAB72105.1	dJ18D14.4 (cytochrome P450, subfamily IVA, polypeptide 11)		253	6.00e-68
		BAC03751.1	unnamed protein product		202	1.00e-52
		AAH28102.1	Unknown (protein for MGC:40051)		202	1.00e-52
NM_009669 NP_033799.1	F:(C-HI) -3.13 U:(C-D) 3.23	NP_000690.1	amylase, alpha 2A; pancreatic; Amylase, pancreatic, alpha-2A			
		NP_066188.1	amylase, alpha 2B; pancreatic; Amylase, pancreatic, alpha-2B		952	0
		XP_086988.1	similar to Alpha-amylase, salivary precursor (1,4-alpha-D-glucan glucanohydrolase)		946	0
		67366	alpha-amylase (EC 3.2.1.1) precursor, salivary - human		941	0
		NP_004029.1	amylase, alpha 1A; salivary; Amylase, salivary, alpha-1A		939	0
		7245760	Chain A, Structure Of Human Pancreatic Alpha-Amylase In Complex With The Carbohydrate Inhibitor Acarbose		939	0
		1421331	Chain , Mol_id: 1; Molecule: Human Pancreatic Alpha-Amylase; Chain: Null; Ec: 3.2.1.1		927	0
		18655894	Chain A, Three Dimensional Structure Analysis Of The R195q Variant Of Human Pancreatic Alpha Amylase		925	0
					924	0

			18655893	Chain A, Three Dimensional Structure Analysis Of The R337q Variant Of Human Pancreatic Alpha-Mylase	924	0
			14719496	Chain A, Subsite Mapping Of The Active Site Of Human Pancreatic Alpha-Amylase Using Substrates, The Pharmacological Inhibitor Acarbose, And An Active Site Variant	923	0
			20664071	Chain A, Mechanistic Analyses Of Catalysis In Human Pancreatic Alpha- Amylase: Detailed Kinetic And Structural Studies Of Mutants Of Three Conserved Carboxylic Acids	923	0
			20664068	Chain A, Three Dimensional Structure Analysis Of The R195a Variant Of Human Pancreatic Alpha Amylase	923	0
			18655892	Chain A, Three Dimensional Structure Analysis Of The R337a Variant Of Human Pancreatic Alpha-Amylase	923	0
			20664074	Chain A, Mechanistic Analyses Of Catalysis In Human Pancreatic Alpha- Amylase: Detailed Kinetic And Structural Studies Of Mutants Of Three Conserved Carboxylic Acids	922	0
			1633119	Chain , Human Salivary Amylase	919	0
			15983375	Chain A, Role Of Mobile Loop In The Mechanism Of Human Salivary Amylase	914	0
			15983376	Chain A, Role Of EtHe Mobile Loop In The Mechanism Of Human Salivary Amylase	904	0
			AA57345.1	alpha-amylase	515	1.00e-146
NM_007643 NP_031669.1	Mm.18628	F:(C-HI) -3.03, U:(C-D) 2.05, U:(HI-D) 3.33	P16671	Platelet glycoprotein IV (GPV) (GPIIB) (CD36 antigen) (PAS IV) (PAS-4 protein)		
			NP_000063.1	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I)	798	0
			I59613	cell adhesion receptor CD36	796	0
			AAM14636.1	CD36 antigen (collagen type I receptor, thrombospondin receptor)	791	0
					780	0

				NP_005497.1	scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor) ; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II)	271	3.00e-72
				A56525	lysosomal integral membrane protein II - human	271	3.00e-72
				NP_005496.2	scavenger receptor class B, member 1; CD36 antigen-like 1; scavenger receptor class B type 1; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	255	2.00e-67
				A48528	membrane glycoprotein CLA-1 protein long form precursor - human	252	2.00e-66
AK007264 BAB24924.1	Mm.20037 0	F:(C-HI) -2.95, U:(HI-D) 2.34		AAD12227.1	similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)		
				XP_087230.2	similar to Uridine phosphorylase (UDRPase)	447	1.00e-125
				NP_003355.1	uridine phosphorylase	428	1.00e-120
NM_010379 NP_034509.1	Mm.6716	F:(C-HI) -2.87, U:(HI-D) 2.37		I54432	MHC class II histocompatibility antigen DQw1-beta chain precursor	316	3.00e-86
				I67725	cell surface glycoprotein - human	347	1.00e-95
				AAA92332.1	MHC class II HLA-DQ-beta-1	347	1.00e-95
				NP_002114.1	major histocompatibility complex, class II, DQ beta 1 precursor	342	4.00e-94
				AAA92331.1	MHC class II HLA-DQ-beta-1	340	1.00e-93
				P05537	HLA class II histocompatibility antigen, DQ(W3) beta chain precursor	340	1.00e-93
				AAB41231.1	MHC class II HLA-DQ	338	5.00e-93
				P01920	HLA class II histocompatibility antigen, DQ(3) beta chain precursor (Clone II-102)	338	5.00e-93
				AAA59768.1	HLA-DQB1	337	1.00e-92
				I55996	MHC HLA-DQ-beta cell surface glycoprotein - human	337	1.00e-92
				AAC41966.1	MHC class II HLA-DQ-beta-1	335	3.00e-92
				AAF28315.1	MHC class II antigen	335	4.00e-92
				AAC41964.1	MHC class II HLA-DQ-beta-1	333	2.00e-91
				AAC41965.1	MHC class II HLA-DQ-beta-1	333	2.00e-91
						332	4.00e-91

			P03992	HLA class II histocompatibility antigen, DQB1*0602 beta chain precursor (DQ(5)) (DC-1)	331	6.00e-91
			AAA59772.1	lymphocyte antigen	329	3.00e-90
			I68718	MHC class II histocompatibility antigen DQ-beta chain precursor - human	328	4.00e-90
			B37044	MHC class II histocompatibility antigen HLA-DQ beta chain (DQ4) precursor - human	328	4.00e-90
			P05538	HLA class II histocompatibility antigen, DX beta chain precursor	328	4.00e-90
			CAA65280.1	human leukocyte antigen-DQ beta chain	328	7.00e-90
			AAC41973.1	MHC class II HLA-DQ-beta-1	328	7.00e-90
			AAC41974.1	MHC class II HLA-DQ-beta-1	327	9.00e-90
NM_020564 NP_065589.1	Mm.6562	F:(C-HI) -2.84, F:(C-D) -2.36, U:(HI-D) 2.6	AAC78553.1	hydroxysteroid sulfotransferase SUL T2B1a		
			NP_004596.1	sulfotransferase family, cytosolic, 2B, member 1; sulfotransferase family 2B, member 1	228	1.00e-59
			AAC78499.1	hydroxysteroid sulfotransferase SUL T2B1b	228	1.00e-59
			21465697	Chain A, Crystal Structure Of Human Dehydroepiandrosterone Sulfotransferase In Complex With Substrate	218	1.00e-56
NM_032400 NP_115776.1	Mm.12511 0	F:(C-HI) -2.79, U:(HI-D) 3.03	AAL95690.1	P2Y purinoceptor 1		
			NP_149039.1	G protein-coupled receptor 91	474	1.00e-133
NM_008495 NP_032521.1	Mm.43831	F:(C-HI) -2.65, U:(C-D) 2.32	NP_002296.1	beta-galactosidase binding lectin precursor; Lectin, galactose-binding, soluble, 1; galeclin	474	1.00e-133
					259	2.00e-69

AK003129	Mm.2368		1713410A	beta galactoside soluble lectin	257	6.00e-69
BAB22589.1		F:(C-HI) -2.51, F:(C-D) -3.41, U:(HI-D) 3.46	AAH00294.1	Unknown (protein for IMAGE:2819455)		
			NP_006326.1	translocase of inner mitochondrial membrane 17 homolog A (yeast); preprotein translocase	241	8.00e-64
					239	3.00e-63
NM_011596	Mm.1158	F:(C-HI) -2.51, F:(C-D) -2.34, U:(HI-D) 4.16	NP_036595.1	TJ6 protein		
NP_035726.1					1479	0
			AAH32398.1	ATPase, H ⁺ transporting, lysosomal V0 subunit a isoform 1	811	0
			NP_005168.2	ATPase, H ⁺ transporting, lysosomal, non-catalytic accessory protein 1A, 110/116 kDa subunit; ATPase, H ⁺ transporting, lysosomal non-catalytic accessory protein 1 (110/116kD); vacuolar proton pump, subunit 1; clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit; vacuolar proton translocating ATPase 116 kDa subunit A isoform 1; vacuolar adenosine triphosphatase subunit Ac116; H(+)-transporting two-sector ATPase, 116 kDa accessory protein A1; vacuolar-type H(+)-ATPase 115 kDa subunit		
			CAA96077.1	vacuolar-type H(+)-ATPase 115 kDa subunit	809	0
					806	0

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			NP_065683.1	ATPase, H ⁺ transporting, lysosomal V0 subunit a isoform 4; vacuolar proton pump 116 kDa accessory subunit; vacuolar proton pump, subunit 2; H(+)-transporting two-sector ATPase, noncatalytic accessory protein 1B; ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B; renal tubular acidosis; ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 2 (38kD)	787	0
			NP_006010.2	T-cell, immune regulator 1, isoform a; ATPase, H ⁺ transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis	766	0
			Q13488	Vacuolar proton translocating ATPase 116 kDa subunit A isoform 3 (V-ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit) (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune response cDNA7 protein) (TIRC7)	764	0
			AAA97878.1	specific 116-kDa vacuolar proton pump subunit	757	0
			AAH22300.1	Unknown (protein for MGC:22527)	640	0
			NP_006044.1	T-cell, immune regulator 1, isoform b; ATPase, H ⁺ transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis	609	1.00e-174
AF193796 AAL09298.1	Mm.20706 2	F:(C-HI) -2.33, U:(HI-D) 3.03	XP_006804.2	similar to Homeobox protein Hox-C13 (Hox-3G)		
			NP_059106.1	homeo box C13	505	1.00e-142
			BAB14786.1	unnamed protein product	504	1.00e-142
					280	7.00e-75

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NM_016704 NP_057913.1	Mm.20247	F:(C-HI) -2.26, U:(HI-D) 3.29	NP_000056.1	Complement component 6 precursor	1249	0
			A34372	complement C6 precursor [validated]	1246	0
			XP_170508.1	similar to Complement component C6 precursor	916	0
			AAB59433.1	complement component C6	760	0
			NP_000578.1	complement component 7 precursor	397	1.00e-110
			CAA60121.1	complement C7	394	1.00e-109
NM_007870 NP_031896.1	Mm.10287	F:(C-HI) -2.2, U:(HI-D) 2.24	NP_004935.1	deoxyribonuclease I-like 3		
			AAC23652.1	DNase gamma	506	1.00e-143
			BAA11841.1	deoxyribonuclease I precursor	504	1.00e-143
			NP_005214.2	deoxyribonuclease I	237	2.00e-62
			NP_001365.1	deoxyribonuclease I-like 2	237	3.00e-62
			NP_006721.1	deoxyribonuclease I-like 1	226	5.00e-59
			AAB00496.1	DNLI gene product	224	1.00e-58
			AAB00495.1	DNase I	224	1.00e-58
			AAD00638.1	Fc-gamma-R1Ib2	221	1.00e-57
NM_010187 NP_034317.1	Mm.10809	F:(C-HI) -2.18, U:(HI-D) 2.55				
			AAD00641.1	Fc-gamma-R1Ib2	309	6.00e-84
			CAA36713.1	precursor polypeptide (AA -42 to 249)	306	6.00e-83
			AAA35842.1	IgG Fc fragment receptor precursor	305	8.00e-83
			AAA36051.1	IgG Fc receptor beta-Fc-gamma-R1I	304	2.00e-82
			CAA35644.1	IgG Fc receptor	301	1.00e-81
			AAD00639.1	Fc-gamma-R1Ib1	301	2.00e-81
					301	2.00e-81

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				AAD00637.1	Fc-gamma-RIIb1		301	2.00e-81
				AAD00640.1	Fc-gamma-RIIb1		297	3.00e-80
				P31994	Low affinity immunoglobulin gamma FC region receptor II-B precursor (FC-gamma RII-B) (FCRII-B) (IGG FC receptor II-B) (FC-gamma-RIIB) (CD32) (CDW32)		297	3.00e-80
				NP_003992.2	Fc fragment of IgG, low affinity IIb, receptor for (CD32); Fc fragment of IgG, low affinity II, receptor for (CD32)		296	4.00e-80
				JL0119	Fc gamma (IgG) receptor IIb precursor - human		296	1.00e-80
NM_007472	Mm.18625	F:(C-HI)		I52366	uterine water channel - human			
NP_031498.1		-2.17, U:(HI-D) 2.38						
				AAH22486.1	aquaporin 1 (channel-forming integral protein, 28kD)		496	1.00e-140
				NP_000376.1	aquaporin 1; aquaporin 1 (channel-forming integral protein, 28kDa); Aquaporin-1 (channel-forming integral protein, 28kDa); Colton blood group		495	1.00e-139
				AAL87136.1	aquaporin 1		488	1.00e-137
				AAC50649.1	channel-like integral membrane protein		293	7.00e-79
				AAC23788.1	aquaporin		276	8.00e-74
				AAC03168.1	putative alternative lens membrane intrinsic protein		238	2.00e-62
				NP_036196.1	major intrinsic protein of lens fiber; aquaporin		233	1.00e-60
				NP_000477.1	aquaporin 2; Aquaporin-2 (collecting duct)		230	9.00e-60
				AAB30268.1	hAQP-CD=collecting duct aquaporin [human, kidney, Peptide, 271 aa]		228	3.00e-59
				I51877	water-channel aquaporin 2 - human		227	7.00e-59
				I64818	water-channel aquaporin 2 - human		227	7.00e-59
				AAC16481.1	aquaporin (water channel protein)		223	1.00e-57
				NP_004019.1	aquaporin 4 C2 isoform; mercurial-insensitive water channel		221	3.00e-57
				NP_001641.1	aquaporin 4 isoform a; mercurial-insensitive water channel		221	3.00e-57
				I39177	mercurial-insensitive water channel - human		221	4.00e-57
				I39178	aquaporin 4, long splice form - human		221	4.00e-57
				NP_001642.1	aquaporin 5; Aquaporin-5		218	5.00e-56

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NM_010024	Mm.19987	F:(C-HI) -2.14, .	NP_001913.2	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2);		
NP_034154.1		F:(C-D) -2.01, U:(HI-D) 2.28		Dopachrome tautomerase (dopachrome delta-isomerase; tyrosinase-related protein 2)	883	0
			CAA35785.1	pre propeptide (AA -24 to 503)	502	1.00e-141
			NP_000541.1	tyrosinase-related protein 1	502	1.00e-141
			CAD13328.1	ba3L8.1 (tyrosinase-related protein 1)	498	1.00e-140
			NP_000363.1	tyrosinase (oculocutaneous albinism IA); Tyrosinase	402	1.00e-112
AF385682	Mm.27242	F:(C-HI) -2.04, U:(HI-D) 2.02	NP_071442.1	EGF-TM7-latrophilin-related protein		
AAK62363.1						
			BAA34488.1	KIAA0768 protein	934	0
			NP_056051.1	lectomedin-3	359	2.00e-98
			AAD54676.1	lectomedin-1 beta	348	4.00e-95
			NP_036434.1	latrophilin 1; KIAA0786 protein; lectomedin-1; latrophilin	341	4.00e-93
			AAD54675.1	lectomedin-1 alpha	341	4.00e-93
			BAA34506.1	KIAA0786 protein	337	8.00e-92
			AAG27461.1	lectomedin-2	330	1.00e-89
			NP_055736.1	lectomedin-2; KIAA0821 protein	330	1.00e-89
			AAH07587.1	Unknown (protein for IMAGE:3162852)	322	2.00e-87
			NP_690880.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform b	281	4.00e-75
			NP_001775.2	CD97 antigen, isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein		
			NP_115960.1	egf-like module-containing mucin-like receptor 3 isoform a	280	2.00e-74
			AAF21974.1	EGF-like module EMR2	278	5.00e-74
			NP_038475.2	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform a	277	8.00e-74
			BAC06146.1	seven transmembrane helix receptor	275	4.00e-73
					275	4.00e-73

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				137225	leucocyte antigen CD97		275	4.00e-73
				NP_510966.1	CD97 antigen, isoform 1 precursor; leukocyte antigen CD97; seven-span transmembrane protein		265	3.00e-70
				AAB36682.1	CD97		265	3.00e-70
				BAC06178.1	seven transmembrane helix receptor		265	3.00e-70
				BAC06133.1	seven transmembrane helix receptor		260	1.00e-68
				P48960	Leucocyte antigen CD97 precursor		260	1.00e-68
				NP_001965.1	egf-like module containing, mucin-like, hormone receptor-like sequence 1; egf-like module containing; mucin-like, hormone receptor-like		259	2.00e-68
				NP_690881.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform c		254	7.00e-67
				NP_690883.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform e		231	6.00e-60
				NP_690882.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform d		231	6.00e-60
				NP_690885.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform g		231	6.00e-60
				NP_690884.1	egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform f		231	6.00e-60
				AAC05172.1	R29368_2		225	4.00e-58
NM_010016	Mm.20236	F:(C-HI)		NP_000565.1	decay accelerating factor for complement (CD55, Cromer blood group system);			
NP_034146.1		-2.04, U:(HI-D) 2.14			Decay-accelerating factor of complement			
				P08174	Complement decay-accelerating factor precursor (CD55 antigen)		367	1.00e-101
				AAA52167.1	decay-accelerating factor precursor		365	1.00e-101
				AAB48622.1	decay-acceleration factor		364	1.00e-100
				A26359	decay-accelerating factor, splice form 1 precursor - human		363	1.00e-100
				23200413	Chain R, Structural Model Of Human Decay-Accelerating Factor Bound To Echovirus 7 From Cryo-Electron Microscopy		355	1.00e-97
				AAL25833.1	decay-accelerating factor 1 ab		308	8.00e-64
				AAL25835.1	decay-accelerating factor 4ab		243	6.00e-64
				AAL25834.1	decay-accelerating factor 3		243	6.00e-64
							242	7.00e-64

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NM_023740 NP_076229.1	Mm.20387	F:(C-HI) -1.7, F:(C-D) -2.35, U:(HI-D) 2.52	AAG23766.1	PP3774		648	0
			AAH08074.1	Similar to RIKEN cDNA 1500015N03 gene.		638	0
			AAH33157.1	similar to Abl-philin 2		523	1.00e-148
			NP_115703.1	hypothetical protein MGC2993		452	1.00e-127
NM_009744 NP_033874.1	Mm.15811	F:(C-D) -4.15, U:(HI-D) 2.11	NP_001697.2	B-cell lymphoma 6 protein; B-cell CLL/lymphoma-6; cys-his2 zinc finger transcription factor BCL5; zinc finger protein 51; lymphoma-associated zinc finger gene on chromosome 3		1337	0
			A48752	B-cell CLL/lymphoma 6 (BCL6) protein		1330	0
			BAC00962.1	BAZF		335	1.00e-91
			XP_171849.1	similar to Bcl6-associated zinc finger protein		300	7.00e-81
NM_008245 NP_032271.1	Mm.33896	F:(C-D) -2.62, U:(HI-D) 2.05	NP_002720.1	hematopoietically expressed homeobox; proline-rich homeodomain-containing transcription factor			
			JN0767	homeobox protein HEX - human		381	1.00e-106
			AAH14336.1	Similar to hematopoietically expressed homeobox		380	1.00e-105
			CAA79730.1	homeobox related protein		379	1.00e-105
NM_008183 NP_032209.1	Mm.14601	F:(C-D) -2.27 U:(C-D) 2.17	XP_002155.1	similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)		395	1.00e-110
			438890	Chain A, Ligand-Free Human Glutathione S-Transferase M1a-1a		394	1.00e-109
			AAA59203.1	glutathione transferase M1		394	1.00e-109

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NP_000839.1	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2	379	1.00e-105
P46439	Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)	379	1.00e-105
NP_000842.2	glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5	378	1.00e-105
NP_000841.1	glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	377	1.00e-104
S32425	glutathione transferase (EC 2.5.1.18) class mu, GSTM4 (version 2) - human	377	1.00e-104
4557966	ain A, Ligand-Free Human Glutathione S-Transferase M2-2 (E.C.2.5.1.18), Monoclinic Crystal Form	377	1.00e-104
AAA57346.1	glutathione transferase M4	376	1.00e-104
6980588	Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase M4- 4 (E.C.2.5.1.18)	376	1.00e-104
494185	Chain , Glutathione S-Transferase (Human, Class Mu) (Gstm2-2) Form A (E.C.2.5.1.18) Mutant With Trp 214 Replaced By Phe (W214f)	373	1.00e-103
CAA48636.1	glutathione S-transferase	351	8.00e-97
NP_671489.1	glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4	340	2.00e-93
AAH17836.1	Similar to glutathione S-transferase M2 (muscle)	338	7.00e-93
XP_042722.1	similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)	329	3.00e-90
AAH08790.1	Unknown (protein for MGC:3704)	329	3.00e-90
5822511	Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form	329	3.00e-90
106129	glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human	326	3.00e-89

			NP_666533.1	glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu	308	1.00e-83
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Master Table 2: Subtable 2A Classes of Favorable Genes/Proteins

Mouse Gene Protein	Behavior	Human Protein Class
NM_007630	F:(HI-D)	
NP_031656.1	-5.28	Cyclin
		Subclass: cyclin B2
		Subclass: cyclin B1; G2/mitotic-specific cyclin B1
NM_007913	F:(HI-D)	
NP_031939.1	-2.66	Early growth response
		Subclass: early growth response 1; G0S30
		Subclass: early growth response 3
AF127033	F:(HI-D)	
AAG02285.1	-2.1	fatty acid synthase; FAS [Homo sapiens]
NM_011169	F:(HI-D)	
NP_035299.1	-2.08	prolactin receptor
		Subclass: prolactin receptor
		Subclass: prolactin receptor isoform delta S1 precursor
		Subclass: prolactin receptor short isoform 1a
		Subclass: intermediate prolactin receptor isoform
NM_013490	F:(HI-D)	
NP_038518.1	-2.04	choline kinase
		Subclass: choline kinase
		Subclass: choline/ethanolamine kinase isoform a
NM_013888	F:(HI-D)	
NP_038916.1	-2.04	J domain containing protein 1
NM_019499	F:(HI-D)	
NP_062372.1	-2.04	MAD2-like 1; MAD2 (mitotic arrest deficient, yeast, homolog)-like 1; mitotic arrest deficient, yeast, homolog-like 1

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NM_011850 NP_035980.1	F:(HI-D) -2.03	short heterodimer partner; orphan nuclear receptor SHP; small heterodimer partner; nuclear receptor subfamily 0, group B, member 2
AF213393 AAF31432.1	F:(HI-D) -2.02	ATP-binding cassette, sub-family A
		Subclass: ATP-binding cassette, sub-family A member 8
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 9
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 10
		Subclass: ATP-binding cassette, sub-family A (ABC1), member 6
NM_013646 NP_038674.1	F:(HI-D) -2.02	RAR-related orphan receptor
		Subclass: RAR-related orphan receptor A, isoform a; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform c; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform b; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor A, isoform d; RAR-related orphan receptor alpha; retinoic acid receptor-related orphan receptor alpha; transcription factor RZR-alpha; ROR-alpha
		Subclass: RAR-related orphan receptor B; RAR-related orphan receptor beta; retinoic acid-binding receptor beta; nuclear receptor RZR-beta
NM_009425 NP_033451.1	F:(HI-D) -10.21	tumor necrosis factor (ligand) superfamily, member 10; Apo-2 ligand; TNF-related apoptosis inducing ligand TRAIL
AK018485 2204249A	F:(C-HI)-2.4 5	hypothetical protein FLJ90165

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NM_008182 NP_032208.1	F:(C-HI) -9.17, F:(C-D) -5.68	glutathione transferase
		Subclass: glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2
		Subclass: TPA: glutathione transferase A5
		Subclass: Chain A, Glutathione S-Transferase A1-1 (E.C.2.5.1.18)
		Subclass: Glutathione S-transferase A3-3 (GST class-alpha)
		Subclass: glutathione S-transferase A3
		Subclass: glutathione transferase (EC 2.5.1.18) alpha-2 (clone GTH2) - human
NM_028089 NP_082365.1	F:(C-HI) -4.31, F:(C-D) -5.26	cytochrome P-450
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
		Subclass: cytochrome P450 2C17

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NM_007818 NP_031844.1	F:(C-HI) -4.29, F:(C-D) -8.15	cytochrome P450
		Subclass: Cytochrome P450 3A4 (Quinine 3-monooxygenase) (CYP3A4) (Nifedipine oxidase) (NF-25) (P450-PCN1)
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 4; nifedipine oxidase; P450-III, steroid inducible; glucocorticoid-inducible P450; cytochrome P450, subfamily IIIA (nifedipine oxidase), polypeptide 3
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 5; nifedipine oxidase; aryl hydrocarbon hydroxylase; xenobiotic monooxygenase; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIIA, polypeptide 7; aryl hydrocarbon hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450 polypeptide 43 isoform 2; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 1; cytochrome P450 polypeptide 43
		Subclass: cytochrome P450 polypeptide 43 isoform 3; cytochrome P450 polypeptide 43
NM_025429 NP_079705.1	F:(C-HI) -3.51, F:(C-D) -3.01	serine (or cysteine) proteinase inhibitor
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)

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NM_008341 NP_032367.1	F:(C-HI) -3.37, F:(C-D) -3.47, F:(HI-D) -2.63	insulin-like growth factor binding protein 1
U38940 AAA85125.1	F:(C-HI) -3.11, F:(C-D) -2.11	asparagine synthetase; glutamine-dependent asparagine synthetase; TS11 cell cycle control protein
J03953 AAA37748.1	F:(C-HI) -3.03	Chain A, ligand-free Glutathione S-Transferase
		Subclass: Chain A, ligand-free, Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: Chain A, Ligand-Free Homodimeric Human Glutathione S-Transferase Mu 4
		Subclass: Chain A, glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-aryltransferase M2
		Subclass: Glutathione S-transferase Mu 5 (GSTM5-5) (GST class-Mu 5)
		Subclass: Similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)
NM_013459 NP_038487.1	F:(C-HI) -2.94	Complement factor D
		Subclass: Complement factor D precursor (C3 convertase activator) (Properdin factor D) (Adipsin)
		Subclass: Chain , Mutant-Of Factor D With Enhanced Catalytic Activity
		Subclass: Chain , Human Complement Factor D In Complex With Isatoic Anhydride Inhibitor

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NM_016810	F:(C-HI)	golgi SNAP receptor complex member 1; Golgi SNARE 28 kDa
NP_058090.1	-2.86	
AK006128	F:(C-HI)	ATP-binding cassette
BAB24422.1	-2.71	Subclass: ATP-binding cassette, sub-family C, member 3 isoform MRP3; canicular multispecific organic anion transporter
		Subclass: multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2)
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 4; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 3; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 1; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 2; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 7; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
		Subclass: ATP-binding cassette, sub-family C, member 1, isoform 6; multiple drug resistance protein 1; multidrug resistance protein; multiple drug resistance-associated protein
NM_008742	F:(C-HI)	neurotrophin 3
NP_032768.1	-2.68	
NM_008361	F:(C-HI)	interleukin 1, beta
NP_032387.1	-2.65,	
	F:(C-D)	
	-2.03	

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AF294617	F:(C-HI)	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase
AAG02118.1	-2.63	
NM_009998	F:(C-HI)	cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6
NP_034128.1	-2.61, F:(C-D)	
	-2.33	
NM_008988	F:(C-HI)	putative neuronal cell adhesion molecule (punc)
NP_033014.1	-2.6	
		Subclass: putative neuronal cell adhesion molecule (punc)
		Subclass: similar to punc
NM_010166	F:(C-HI)	Eyes absent homolog
NP_034296.1	-2.57	
		Subclass: Eyes absent homolog 3 (EYA3)
		Subclass: eyes absent homolog 4 (Drosophila);
		Subclass: eyes absent 1 isoform b; Eyes absent, Drosophila, homolog of, 1; Melnick-Fraser syndrome
		Subclass: EYA1A
		Subclass: Eyes absent homolog 2
		Subclass: EYA1D
AK002480	F:(C-HI)	cystathionase isoform 1; cystathionine gamma-lyase; homoserine deaminase; homoserine dehydratase; cysteine
NP_666065.1	-2.55, F:(C-D)	desulhydrase
	-2.57	

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AK018226 XP_110043.1	F:(C-HI) -2.53, F:(C-D) -2.4	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)
NM_010361 NP_034491.1	F:(C-HI) -2.46, F:(C-D) -2.25	glutathione S-transferase
		Subclass: glutathione S-transferase theta 2
		Subclass: glutathione S-transferase theta 1
AK018485 BAB31233.1	F:(C-HI) -2.46	similar to data source:SPTR, source key:Q60928, evidence:ISS~putative~similar to GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE) (GGT)
		Alternate: hypothetical protein FLJ90165
NM_010924 NP_035054.1	F:(C-HI) -2.45, F:(C-D) -2.19	nicotinamide N-methyltransferase
NM_021307 NP_067282.1	F:(C-HI) -2.44	Zinc finger protein

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		Subclass: zinc finger protein 228	
		Subclass: similar to ZNF228 protein	
		Subclass: Zinc finger protein 226	
		Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein-93 homolog (mouse)	
		Subclass: Hypothetical zinc finger-like protein	
		Subclass: similar to Zinc finger protein 229	
		Subclass: Zinc finger protein ZNF45	
NM_008295	F:(C-HI)		hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1; Hydroxy-delta-5-steroid dehydrogenase, 3 beta-
NP_032321.1	-2.43, F:(C-D) -5.64, F:(HI-D) -2.32		and steroid
NM_010001	F:(C-HI)	cytochrome P450	
NP_034131.1	-2.43, F:(C-D) -2.56		
		Subclass: Cytochrome P450 2C18 (CYP11C18) (P450-6B/29C)	
		Subclass: cytochrome P450 2C19	
		Subclass: cytochrome P450 2C9	
		Subclass: cytochrome P450 2C10	
		Subclass: cytochrome P450 2C8	

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AK012213	F:(C-HI)	aldehyde dehydrogenase 1 family
BAB28101.1	-2.39, F:(C-D) -2.05	
		Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5
		Subclass: Aldehyde dehydrogenase X, mitochondrial precursor (ALDH class 2)
		Subclass: Aldehyde dehydrogenase 1A2 (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-2)
		Subclass: Aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
		Subclass: Aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6
NM_023154	F:(C-HI)	Similar to RIKEN cDNA 0610025L15 gene product
NP_075643.1	-2.39, F:(C-D) -2.48	
NM_010401	F:(C-HI)	histidine ammonia-lyase; Histidine ammonia-lyase (histidase)
NP_034531.1	-2.39, F:(C-D) -2.21	
NM_023455	F:(C-HI)	putative N-acetyltransferase Camello 2
NP_075944.1	-2.39, F:(C-D) -2.04	
		Alternate: N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
		Alternate: GLA
		Alternate: kidney- and liver-specific gene product
		Alternate: hypothetical protein TSC501

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NM_018779 NP_061249.1	F:(C-HI) -2.35, F:(C-D) -2.43	phosphodiesterase
		Subclass: phosphodiesterase 3A, cGMP-inhibited
		Subclass: phosphodiesterase 3B, cGMP-inhibited
AK009563 BAB26361.1	F:(C-HI) -2.33	similar to RIKEN cDNA 2310032D16
		Alternate: KIAA1434 protein
NM_009466 NP_033492.1	F:(C-HI) -2.32, F:(C-D) -2.00	UDP-glucose dehydrogenase (uridine diphosphoglucose dehydrogenase)
NM_013584 NP_038612.1	F:(C-HI) -2.31, F:(C-D) -2.46	leukemia inhibitory factor receptor, LIF receptor [human, placenta, Peptide, 1078 aa]
NM_008061 NP_032087.1	F:(C-HI) -2.28, F:(C-D) -2.14	glucose-6-phosphatase, catalytic

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NM_025631 NP_079907.1	F:(C-HI) -2.25, F:(C-D) -2.16	hypothetical protein dJ726C3.2
NM_025631 NP_079907.1	F:(C-HI) -2.25, F:(C-D) -2.16	hypothetical protein dJ726C3.2
NM_025404 NP_079680.1	F:(C-HI) -2.24, F:(C-D) -2.03	ADP-ribosylation factor
		Subclass: ADP-ribosylation factor 4-like; ADP-ribosylation factor-like 6
		Subclass: similar to ADP-ribosylation-like 4
		Subclass: ADP-ribosylation factor-like 7
		Subclass: ADP ribosylation factor-like protein
NM_008615 NP_032641.1	F:(C-HI) -2.22	NADP-dependent malic enzyme
		Subclass: cytosolic malic enzyme 1; malic enzyme, cytoplasmic; malic enzyme 1, soluble; NADP-dependent malic enzyme; malate dehydrogenase; pyruvic-malic carboxylase
		Subclass: malic enzyme 3, NADP(+)-dependent, mitochondrial; malic enzyme, NADP+-dependent, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase; NADP-ME
		Subclass: malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochondrial; malic enzyme 2, mitochondrial; pyruvic-malic carboxylase; malate dehydrogenase

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NM_026104	F:(C-HI)	similar to RIKEN cDNA 1700095F04 gene product
NP_080380.1	-2.22	
		Alternate: unnamed protein product
NM_008792	F:(C-HI)	proprotein convertase
NP_032818.1	-2.19	Subclass: proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5
		Subclass: proprotein convertase subtilisin/kexin type 1 preproprotein; prohormone convertase 3; prohormone convertase 1; neuroendocrine convertase 1; proprotein convertase 1
NM_013743	F:(C-HI)	pyruvate dehydrogenase kinase
NP_038771.1	-2.19	
		Subclass: pyruvate dehydrogenase kinase, isoenzyme 4
		Subclass: pyruvate dehydrogenase kinase, isoenzyme 1
		Subclass: pyruvate dehydrogenase kinase, isoenzyme 2
		Subclass: pyruvate dehydrogenase kinase, isoenzyme 3
NM_010357	F:(C-HI)	Glutathione S-transferase
NP_034487.1	-2.17, F:(C-D)	
	-2.93	
		Subclass: Glutathione S-transferase A3-3 (GST class-alpha)
		Subclass: glutathione S-transferase A3
		Subclass: glutathione S-transferase A1; GST, class alpha, 1; glutathione S-alkyltransferase A1; glutathione S-aryltransferase A1; S-(hydroxyalkyl)glutathione lyase A1; glutathione S-alkyltransferase A1; GST-epsilon; glutathione S-transferase 2
		Subclass: glutathione S-transferase A2; glutathione S-transferase 2; GST, class alpha, 2; liver GST2; glutathione S-alkyltransferase A2; glutathione S-aryltransferase A2; S-(hydroxyalkyl)glutathione lyase A2; glutathione S-alkyltransferase A2; GST-gamma; HA subunit 2
		Subclass: Chain A, Glutathione Transferase A1-1 Complexed With An Ethacrynic Acid Glutathione Conjugate (Mutant R15k)
		Subclass: TPA: glutathione transferase A5

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			Subclass: glutathione S-transferase A4; glutathione S-alkyltransferase A4; glutathione S-aryltransferase A4; S-(hydroxyalkyl)glutathione lyase A4; glutathione S-alkyltransferase A4; glutathione transferase A4-4; GST class-alpha; glutathione S-transferase, alpha 4
NM_011146	F:(C-HI)		
NP_035276.1	-2.17		peroxisome proliferative activated receptor gamma
			peroxisome proliferative activated receptor gamma, isoform 2; PPAR-gamma; peroxisome proliferator activated receptor gamma
			peroxisome proliferative activated receptor gamma, isoform 1; PPAR-gamma; peroxisome proliferator activated receptor gamma
NM_007395	F:(C-HI)		
NP_031421.1	-2.16		activin A type IB receptor
			Subclass: activin A type IB receptor precursor; serine(threonine) protein kinase
			Subclass: activin A type IB receptor, isoform b precursor; serine(threonine) protein kinase
			Subclass: activin type I receptor SKR2, splice form 2
			Subclass: activin A type IB receptor, isoform c precursor; serine(threonine) protein kinase
			Subclass: activin type I receptor SKR2 splice form 3
			Subclass: transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa); transforming growth factor beta receptor I (activin A receptor type II-like kinase, 53kD)
NM_009127	F:(C-HI)		
NP_033153.1	-2.15,		
	F:(C-D)		
	-3.29,		
	F:(HI-D)		
	-2.71		Acyl-CoA desaturase (Stearoyl-CoA desaturase) (Fatty acid desaturase) (Delta(9)-desaturase)

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NM_007824 NP_031850.1	F:(C-HI) -2.14, F:(C-D) -3.09	Cytochrome P450
		Subclass: Cytochrome P450 7A1 (Cholesterol 7-alpha-monooxygenase) (CYPVII) (Cholesterol 7-alpha-hydroxylase)
		Subclass: cytochrome P450, subfamily VIIIb, polypeptide 1; 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol 12-alpha-
		Subclass: sterol 12-alpha hydroxylase CYP8B1
AK002979 BAB22492.1	F:(C-HI) -2.14, F:(C-D) -2.15	calcyon
AK002979 BAB22492.1	F:(C-HI) -2.14, F:(C-D) -2.15	calcyon
NM_011817 NP_035947.1	F:(C-HI) -2.13	growth arrest and DNA damage inducible protein gamma (GADD45-gamma)
NM_027000 NP_081276.1	F:(C-HI) -2.13	similar to Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein NGB)
		Alternate: G protein-binding protein CRFG; GTP-binding protein
		Alternate: G protein-binding protein CRFG
		Alternate: putative G-binding protein
		Alternate: unnamed protein product

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NM_007815 NP_031841.1	F:(C-HI) -2.11, F:(C-D) -2.78	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase),
		Subclass: Cytochrome P450 2C18 (CYP1IC18) (P450-6B/29C)
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17
		Subclass: cytochrome P450, subfamily IIC, polypeptide 8 isoform 1; mephenytoin 4-hydroxylase; microsomal monooxygenase xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form 1
		Subclass: Cytochrome P450 2C10 (CYP1IC10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
AK006487 BAB24612.1	F:(C-HI) -2.1	hypothetical protein BC015148
NM_008587 NP_032613.1	F:(C-HI) -2.1	c-mer proto-oncogene tyrosine kinase
NM_007912 NP_031938.1	F:(C-HI) -2.09, F:(C-D) -2.69	Epidermal growth factor receptor
		Subclass: epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian); epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Epidermal growth factor receptor
		Subclass: p110 epidermal growth factor receptor
		Subclass: v-erb-a erythroblastic leukemia viral oncogene homolog 4; avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 4; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4

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			Subclass: v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian); Transformation gene ERBB-3; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
			Subclass: Receptor protein-tyrosine kinase erbB-3 (c-erbB3) (Tyrosine kinase-type cell surface receptor HER3)
			Subclass: v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog; Avian erythroblastic leukemia viral (v-erb-b2) oncogene homolog 2; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)
			Subclass: Similar to v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
			Subclass: herstatin
NM_010145	F:(C-HI)		epoxide hydrolase 1, microsomal (xenobiotic); Epoxide hydrolase 1, microsomal (xenobiotic)
NP_034275.1	-2.09,		
	F:(C-D)		
	-2.09		
NM_009676	F:(C-HI)		aldehyde oxidase 1
NP_033806.1	-2.08		
NM_010012	F:(C-HI)		cytochrome P450, subfamily VIIIb, polypeptide 1 (CYP8B1); 7 alpha-hydroxy-4-cholesten-3-one 12-alpha-hydroxylase; sterol
NP_034142.1	-2.08		12-alpha-hydroxylase
NM_011921	F:(C-HI)		aldehyde dehydrogenase 1
NP_036051.1	-2.08		
			Subclass: aldehyde dehydrogenase 1A1; aldehyde dehydrogenase 1, soluble; aldehyde dehydrogenase, liver cytosolic; ALDH class 1; acetaldehyde dehydrogenase 1; retinal dehydrogenase 1
			Subclass: aldehyde dehydrogenase 1 family, member A2; retinaldehyde dehydrogenase 2
			Subclass: aldehyde dehydrogenase 1A3; aldehyde dehydrogenase 6
			Subclass: aldehyde dehydrogenase 1 family, member B1; aldehyde dehydrogenase 5

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NM_018776 NP_061246.1	F:(C-HI) -2.07, F:(C-D) -2.11	cytokine receptor related protein
		Subclass: cytokine receptor related protein 4
		Subclass: cytokine receptor-like factor 3
		Subclass: cytokine receptor-like molecule 9
NM_007474 NP_031500.1	F:(C-HI) -2.07	aquaporin 8
NM_023737 NP_076226.1	F:(C-HI) -2.07	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
AK005535 BAB24106.1	F:(C-HI) -2.06, F:(C-D) -2.16	solute carrier family 39 (zinc transporter), member 4
NM_009864 NP_033994.1	F:(C-HI) -2.05	Cadherin
		Subclass: cadherin 1, type 1 preproprotein; calcium-dependent adhesion protein, epithelial; cadherin 1, E-cadherin (epithelial); uvomorulin; cell-CAM 120/80; Arc-1
		Subclass: E-cadherin
		Subclass: cadherin 3, type 1 preproprotein; P-cadherin; placental cadherin; cadherin 3, P-cadherin (placental); calcium-dependent adhesion protein, placental
		Subclass: cadherin 2, type 1 preproprotein; N-cadherin 1; cadherin 2, N-cadherin (neuronal); neural cadherin; calcium-dependent adhesion protein, neuronal
		Subclass: cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-cadherin; retinal cadherin
		Subclass: Cadherin-4 precursor (Retinal-cadherin) (R-cadherin) (R-CAD)

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			Alternate: uvomorulin	
NM_023341	F:(C-HI)		chaperone	
NP_075830.1	-2.05			
			Subclass: chaperone-ABC1-like	
			Subclass: chaperone, ABC1 activity of bc1 complex like	
			Alternate: unnamed protein product	
AF071068	F:(C-HI)			
AAC25566.1	-2.04, F:(C-D)			
	-2.29		decarboxylase	
			Subclass: dopa decarboxylase (aromatic L-amino acid decarboxylase); aromatic L-amino acid decarboxylase	
			Subclass: Histidine decarboxylase (HDC)	
NM_009263	F:(C-HI)		Osteopontin	
NP_033289.1	-2.04			
			Subclass: Osteopontin precursor (Bone sialoprotein 1) (Urinary stone protein) (Secreted phosphoprotein 1) (SPP-1) (Nephroptin) (Uropontin)	
			Subclass: OPN-a	
			Subclass: OPN-b	
			Subclass: OPN-c	
			carboxylesterase	
NM_053200	F:(C-HI)			
NP_444430.1	-2.04			
			Subclass: carboxylesterase 3; brain carboxylesterase BR3	
			Subclass: brain carboxylesterase hBr2	
			Subclass: carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)	

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			Subclass: Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)
			Subclass: serine esterase N-terminal truncated (503 AA)
			Subclass: brain carboxylesterase hBr1
			Subclass: Alternate: acyl coenzyme A:cholesterol acyltransferase
AK007964	F:(C-HI)		cholinephosphotransferase 1
BAB25375.1	-2.03, F:(C-D)		
	-2.36		
NM_009748	F:(C-HI)		Golgi vesicular membrane trafficking protein p18; Bet1 (S. cerevisiae) homolog; Bet1p homolog
NP_033878.1	-2.03, F:(C-D)		
	-2.15		
NM_019811	F:(C-HI)		acetyl-CoA synthetase
NP_062785.1	-2.03, F:(C-D)		
	-2.11		
			Subclass: acetyl-CoA synthetase isoform a; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
			Subclass: acetyl-CoA synthetase isoform b; cytoplasmic acetyl-coenzyme A synthetase; acetate-CoA ligase; acyl-activating enzyme; acetate thiokinase; acetyl-CoA synthetase
NM_011834	F:(C-HI)		L-kynurenine/alpha-aminoacidipate aminotransferase; kynurenine aminotransferase II
NP_035964.1	-2.03		
			Alternate: Similar to L-kynurenine/alpha-aminoacidipate aminotransferase

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NM_009221 NP_033247.1	F:(C-HI) -2.02	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor
NM_011125 NP_035255.1	F:(C-HI) -2.01	phospholipid transfer protein
		Alternate: Similar to phospholipid transfer protein
NM_010062 NP_034192.1	F:(C-HI) -2.00, F:(C-D) -2.4	deoxyribonuclease
		Subclass: deoxyribonuclease II, lysosomal; DNase II, lysosomal
		Subclass: deoxyribonuclease II beta, isoform 1 precursor; DNase II-like acid DNase; endonuclease DLAD
NM_007811 NP_031837.1	F:(C-HI) -17.03, F:(C-D) -3.81	Cytochrome P450 26 (Retinoic acid-metabolizing cytochrome) (P450RAI) (hP450RAI) (Retinoic acid 4-hydroxylase)
NM_053215 NP_444445.1	F:(C-HI) -1.98, F:(C-D) -3.23	UDP glycosyltransferase; UDP-glucuronyltransferase
		Subclass: UDP glycosyltransferase 2 family, polypeptide B17; UDP-glucuronyltransferase, family 2, beta-17
		Subclass: similar to UDP-glucuronosyltransferase 2B15 precursor, microsomal (UDPGT) (UDPGTH-3) (HLUG4)
		Subclass: UDP glycosyltransferase 2 family, polypeptide B15; UDP-glucuronyltransferase, family 2, beta-15
		Subclass: UDP glycosyltransferase 2 family, polypeptide B4; UDP-glucuronyltransferase, family 2, beta-4
		Subclass: similar to UDP-glucuronosyltransferase 2B4 precursor, microsomal (UDPGT) (Hydoxychoic acid) (HLUG25) (UDPGTH-1)
		Subclass: UDP glycosyltransferase 2 family, polypeptide B7; UDP-glucuronyltransferase, family 2, beta-7

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			Subclass: UDP glycosyltransferase 2 family, polypeptide A1; UDP glucuronosyltransferase 2 family, polypeptide A1
			Subclass: UDP glycosyltransferase 2 family, polypeptide B11
			Subclass: UDP glycosyltransferase 2 family, polypeptide B10
			Subclass: UDP glycosyltransferase 2 family, polypeptide B28
NM_022411			
NP_071856.1	F:(C-D)-5.5 6	transporter protein	
			Subclass: sodium/sulfate symporter/sodium/sulphate symporter
			Subclass: solute carrier family 13 (sodium/sulfate symporters), member 1; solute carrier family 13 (sodium/sulphate symporters), member 1
			Subclass: solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2; sodium-coupled citrate transporter
			Subclass: Solute carrier family 13, member 3 (Sodium-dependent high-affinity dicarboxylate transporter 2) (Na(+)/dicarboxylate cotransporter 3) (NaDC-3) (hNaDC3).
			Subclass: Solute carrier family 13, member 4 (Na+/sulfate cotransporter SUT-1).
			Subclass: Na+-coupled citrate transporter protein
NM_018866			
NP_061354.1	F:(C-D)-3.5 2	chemokine	
			Subclass: chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant); B-cell-homing chemokine (ligand for Burkitt's lymphoma receptor-1); small inducible cytokine B subfamily (Cys-X-Cys motif), member 13 (B-cell chemoattractant)
NM_009270			
NP_033296.1	F:(C-D)-3.4 4	Enzymes involved in hepatic cholesterol synthesis	

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			Subclass: squalene monooxygenase
			Subclass: squalene epoxidase
NM_017379			
NP_059075.1	F:(C-D)-3.1	tubulin	
		Subclass: alpha tubulin	
		Subclass: tubulin, alpha, ubiquitous	
		Subclass: tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain	
		Subclass: tubulin, alpha-like 2; tubulin, alpha 8	
		Subclass: tubulin, alpha 2 isoform 1	
		Subclass: tubulin, alpha 2 isoform 2	
		Subclass: tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tub2	
		Subclass: tubulin alpha 6	
		Subclass: tubulin beta	
		Subclass: Tubulin beta-1 chain	
		Subclass: tubulin, beta, 2	
		Subclass: Tubulin beta-4 chain (Tubulin beta-III).	
		Subclass: tubulin beta-5	
		Subclass: tubulin gamma	
		Subclass: Tubulin gamma-1 chain (Gamma-1 tubulin) (Gamma-tubulin complex component 1) (GCP-1).	
		Subclass: tubulin, gamma 2	
		Subclass: tubulin epsilon	
		Subclass: tubulin, epsilon 1; epsilon-tubulin	
	F:(C-D)-2.8		
AK005060			
P29758	F:(C-HI)-2.6	alanine-glyoxylate aminotransferase	
		Subclass: alanine-glyoxylate aminotransferase 2-like 1	

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			Subclass: alanine-glyoxylate aminotransferase 2 precursor; beta-alanine-pyruvate aminotransferase; beta-ALAAAT II
NM_021475			
NP_067450.1	F:(C-D)-2.7 4		metalloproteinase
			Subclass: disintegrin and metalloproteinase
			Subclass: a disintegrin and metalloproteinase domain 28 isoform 1 preproprotein
			Subclass: a disintegrin and metalloproteinase domain 28 isoform 2 preproprotein
			Subclass: a disintegrin and metalloproteinase domain 28 isoform 3 preproprotein
			Subclass: ADAM 7 precursor (A disintegrin and metalloproteinase domain 7) (Sperm maturation-related glycoprotein GP-83).
			Subclass: a disintegrin and metalloproteinase domain 8 precursor
			Subclass: a disintegrin and metalloproteinase domain 9 preproprotein; meltrin gamma
			Subclass: a disintegrin and metalloproteinase domain 33 isoform beta preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloprotease disintegrin
			Subclass: a disintegrin and metalloproteinase domain 33 isoform alpha preproprotein; disintegrin and reprolysin metalloproteinase family protein; metalloprotease disintegrin
			Subclass: disintegrin protease; ADAM-like protein decysin 1
NM_007703			
NP_031729.1	F:(C-D)-2.7 1		Enzymes that elongate long chain fatty acids
			Subclass: elongation of very long chain fatty acids like 3
			Subclass: CIG30
			Subclass: ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast); long-chain fatty-acyl elongase

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NM_013878		
NP_038906.1	F:(C-D)-2.6 3	calcium binding protein
		Subclass: calcium binding protein 2
		Subclass: calcium binding protein 2 isoform 1; CaBP2
		Subclass: calcium binding protein 2 isoform 2; CaBP2
		Subclass: calcium binding protein 1
		Subclass: calcium binding protein 1 isoform 1; calbrain; calcium binding protein 5; calcium binding protein 1; calbrain
		Subclass: calcium binding protein 1 isoform 2; calbrain; calcium binding protein 5; calcium binding protein 1; calbrain
		Subclass: calcium binding protein 4
		Subclass: calcium binding protein 5
NM_011087		
NP_035217.1	F:(C-D)-2.4 9	Receptor
		Subclass: leucocyte immunoglobulin-like receptor
		Subclass: leucocyte immunoglobulin-like receptor-3; LIR-3
		Subclass: leucocyte immunoglobulin-like receptor, subfamily A
		Subclass: leucocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1; leukocyte immunoglobulin-like receptor 6
		Subclass: leucocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2; leukocyte immunoglobulin-like receptor 7
		Subclass: leucocyte immunoglobulin-like receptor, subfamily A, member 5; immunoglobulin-like transcript 10 ..
		Subclass: leucocyte immunoglobulin-like receptor, subfamily B
		Subclass: leucocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5
		Subclass: leucocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; leukocyte immunoglobulin-like receptor 2

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			Subclass: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 6; immunoglobulin-like transcript 8
			Subclass: leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1; leukocyte immunoglobulin-like receptor 1; CD85 antigen
5			Subclass: leukocyte immunoglobulin-like receptor 1
			Subclass: leukocyte immunoglobulin-like receptor-2
			Subclass: leukocyte immunoglobulin-like receptor-4; LIR-4
			Subclass: immunoglobulin-like transcript 5 protein, ILT5
			Subclass: immunoglobulin-like transcript 6
			Subclass: immunoglobulin-like transcript 7; ILT7
			Subclass: killer cell inhibitory receptor p91 precursor
10			Subclass: monocyte inhibitory receptor precursor
	NM_010849		
15	NP_034979.2	F:(C-D)-2.4 5	v-myc myelocytomatosis viral oncogene homolog; Avian myelocytomatosis viral (v-myc) oncogene homolog; C-MYC; v-myc avian myelocytomatosis viral oncogene homolog
	NM_009414		
20	NP_033440.1	F:(C-D)-2.4 2	hydroxylase
			Subclass: tryptophan hydroxylase
			Subclass: tryptophan hydroxylase 1 (tryptophan 5-monooxygenase); tryptophan hydroxylase (tryptophan 5-monooxygenase)
			Subclass: neuronal tryptophan hydroxylase
			Subclass: phenylalanine hydroxylase
25			Subclass: tyrosine hydroxylase
			Subclass: hydroxylase 2, Tyr
			Subclass: hydroxylase 3, Tyr

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NM_008039			
NP_032065.1	F:(C-D)-2.4	Receptor	
		Subclass: formyl peptide receptor	
		Subclass: formyl peptide receptor-like 1; lipoxin A4 receptor (formyl peptide receptor related)	
		Subclass: formyl peptide receptor-like 2	
		Subclass: fMet-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)(FPR) (N-formyl peptide chemoattractant receptor).	
		Subclass: N-formyl peptide receptor	
		Subclass: N-formylpeptide receptor fMLP-R98	
		Subclass: orphan G-protein coupled receptor Dez isoform a	
		Subclass: chemokine-like receptor	
		Subclass: Chemokine receptor-like 1 (G-protein coupled receptor DEZ) (G protein-coupled receptor ChemR23).	
NM_023142			
NP_075631.1	F:(C-D)-2.3 9	actin related protein	
		Subclass: actin related protein 2/3 complex subunit 1A; actin binding protein (Schizosaccharomyces pombe sop2-like); SOP2-like protein	
		Subclass: actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex subunit p41; actin related protein 2/3 complex subunit 1A (41 kD)	
NM_007864			
NP_031890.1	F:(C-D)-2.3 8	Presynaptic protein	
		Subclass: Presynaptic protein SAP97 (Synapse-associated protein 97) (Discs, large homolog 1) (hDlg).	

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			Subclass: discs, large homolog 2, chapsyn-110; chapsyn-110
			Subclass: discs, large, homolog 3; neuroendocrine-dlg
			Subclass: discs, large (Drosophila) homolog 4
			Subclass: KIAA1232 protein
			Subclass: Tax interaction protein 15
			Subclass: post-synaptic density 95
	NM_010098		
10	NP_034228.1	F:(C-D)-2.3 6	extraretinal photoreceptor
			Subclass: Opsin (encephalopsin, panopsin)
			Subclass: opsin 3 (encephalopsin, panopsin); opsin 3 (encephalopsin)
			Subclass: encephalopsin splice variant 1-2-5-6
15	NM_010206		
	NP_034336.1	F:(C-D)-2.3 5	Receptor
			Subclass: Receptor tyrosine kinase
			Subclass: Growth Factor Receptor tyrosine kinase
20			Subclass: fibroblast growth factor receptor
			Subclass: fibroblast growth factor receptor 1
			Subclass: fibroblast growth factor receptor 1 isoform 1 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
			Subclass: fibroblast growth factor receptor 1 isoform 2 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
25			Subclass: similar to fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)

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		Subclass: fibroblast growth factor receptor 1 isoform 3 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 1 isoform 4 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 1 isoform 5 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 1 isoform 6 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 1 isoform 7 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 1 isoform 9 precursor; fms-related tyrosine kinase-2; heparin-binding growth factor receptor; FMS-like tyrosine kinase 2; basic fibroblast growth factor receptor 1; N-sam tyrosine kinase; FLG protein; protein-tyrosine kinase; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2
		Subclass: fibroblast growth factor receptor 2 isoform 1 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 2 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase

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		Subclass: fibroblast growth factor receptor 2 isoform 4 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 5 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 6 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 7 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 8 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 9 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 10 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 11 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 2 isoform 12 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase

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		Subclass: fibroblast growth factor receptor 2 isoform 13 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 3
		Subclass: fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4
		Subclass: fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4
		Subclass: fibroblast growth factor 4
		Subclass: fibroblast growth factor receptor 4 isoform 1 precursor; tyrosine kinase related to fibroblast growth factor receptor; tyrosylprotein kinase; protein-tyrosine kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 4 isoform 2 precursor; tyrosine kinase related to fibroblast growth factor receptor; tyrosylprotein kinase; protein-tyrosine kinase; hydroxyaryl-protein kinase
		Subclass: fibroblast growth factor receptor 4, soluble-form splice variant
		Subclass: keratinocyte growth factor receptor
		Subclass: keratinocyte growth factor receptor 2 isoform K-sam-1IC3
		Subclass: keratinocyte growth factor receptor 2 isoform KGFR
		Subclass: keratinocyte growth factor receptor 2 isoform BEK
		Subclass: heparin-binding growth factor receptor
		Subclass: heparin-binding growth factor receptor variant alpha-a2
		Subclass: heparin-binding growth factor receptor K-sam precursor
		Subclass: RET tyrosine kinase receptor
		Subclass: ret proto-oncogene isoform c; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET
		Subclass: ret proto-oncogene (multiple endocrine neoplasia MEN2A, MEN2B and medullary thyroid carcinoma 1, Hirschsprung disease)
		Subclass: ret proto-oncogene isoform b; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET
		Subclass: ret proto-oncogene isoform a; RET transforming sequence; hydroxyaryl-protein kinase; cadherin family member 12; oncogene RET
		Subclass: vascular endothelial growth factor receptor
		Subclass: vascular endothelial growth factor receptor 2

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			Subclass: TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)
			Subclass: insulin-like growth factor I receptor, IGF-IR [human, Peptide, 1367 aa].
NM_011781			metalloprotease/disintegrin-like protein (ADAM)
NP_035911.1	F:(C-D)-2.3 3		
			Subclass: ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)(Fertilin beta subunit) (PH-30) (PH30).
			Subclass: ADAM 7 precursor (A disintegrin and metalloproteinase domain 7) (Sperm maturation-related glycoprotein GP-83).
			Subclass: a disintegrin and metalloproteinase domain 8 precursor
			Subclass: disintegrin/metalloproteinase domain 9 short protein precursor
			Subclass: ADAM 11 precursor (A disintegrin and metalloproteinase domain 11) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein) (MDC).
			Subclass: a disintegrin and metalloprotease domain 11 isoform 1 preproprotein; metalloproteinase-like, disintegrin-like, cysteine-rich protein
			Subclass: a disintegrin and metalloprotease domain 11 isoform 2 preproprotein; metalloproteinase-like, disintegrin-like, cysteine-rich protein
			Subclass: a disintegrin and metalloprotease domain 12 isoform 1 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha
			Subclass: a disintegrin and metalloprotease domain 12 isoform 2 preproprotein; A disintegrin and metalloproteinase domain 12 (Meltrin-alpha, mouse, homolog of); meltrin alpha
			Subclass: disintegrin-like metalloproteinase MDC15
			Subclass: a disintegrin and metalloproteinase domain 18 proprotein
			Subclass: ADAM 19 precursor (A disintegrin and metalloproteinase domain 19) (Meltrin beta) (Metalloprotease and disintegrin dentritic antigen marker) (MADDAM).
			Subclass: a disintegrin and metalloproteinase domain 19 isoform 1 preproprotein; meltrin beta
			Subclass: a disintegrin and metalloproteinase domain 19 isoform 2 preproprotein; meltrin beta
			Subclass: ADAM 20 precursor (A disintegrin and metalloproteinase domain 20).
			Subclass: ADAM 21; testis-specific metalloprotease-like membrane protein
			Subclass: a disintegrin and metalloproteinase domain 22

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		Subclass: a disintegrin and metalloproteinase domain 22 isoform 1 proprotein; MDC2 delta
		Subclass: a disintegrin and metalloproteinase domain 22 isoform 2 proprotein; MDC2 delta
		Subclass: a disintegrin and metalloproteinase domain 22 isoform 3 proprotein; MDC2 delta
		Subclass: a disintegrin and metalloproteinase domain 22 isoform 4 proprotein; MDC2 delta
		Subclass: a disintegrin and metalloproteinase domain 22 isoform 5 proprotein; MDC2 delta
		Subclass: a disintegrin and metalloproteinase domain 23 preproprotein
		Subclass: a disintegrin and metalloproteinase domain 28
		Subclass: a disintegrin and metalloproteinase domain 28 isoform 1 preproprotein
		Subclass: a disintegrin and metalloproteinase domain 28 isoform 2 preproprotein
		Subclass: a disintegrin and metalloproteinase domain 28 isoform 3 preproprotein
		Subclass: ADAM 29 precursor (A disintegrin and metalloproteinase domain 29).
		Subclass: a disintegrin and metalloproteinase domain 29 isoform 1 preproprotein
		Subclass: a disintegrin and metalloproteinase domain 29 isoform 2 preproprotein
		Subclass: a disintegrin and metalloproteinase domain 29 isoform 3 preproprotein
		Subclass: ADAM 30 precursor (A disintegrin and metalloproteinase domain 30).
		Subclass: a disintegrin and metalloproteinase domain 33
		Subclass: a disintegrin and metalloproteinase domain 33 isoform alpha preproprotein; disintegrin and reprotolysin metalloproteinase family protein; metalloprotease disintegrin
		Subclass: a disintegrin and metalloproteinase domain 33 isoform beta preproprotein; disintegrin and reprotolysin metalloproteinase family protein; metalloprotease disintegrin
		Subclass: fertilin beta
NM_011461		
NP_035591.	F:(C-D)-2.3	
2	1	hypothetical protein MGC40611

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NM_009021			
NP_033047.1	F:(C-D)-2.2 7	retinoic-acid induced protein	
		Subclass: retinoic-acid induced protein 1	
		Subclass: retinoic acid induced 1 isoform 1	
		Subclass: retinoic acid induced 1 isoform 2	
		Subclass: retinoic acid induced 1 isoform 3	
		Subclass: KIAA1820 protein	
		Subclass: hypothetical protein DKFZp434A139.1 - human	
NM_021468			
NP_067443.1	F:(C-D)-2.1 8	UNC13 (C. elegans)-like; homolog of rat Munc13 (diacylglycerol-binding)	
		Alternate: KIAA1032 protein	
X03796	F:(C-D)-2.1 4	Aldolase	
CAA27422.1		Subclass: aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase	
		Subclass: aldolase B, fructose-bisphosphate; Aldolase B, fructose-bisphosphatase	
		Subclass: aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase	
NM_007489			
NP_031515.1	F:(C-D)-2.1 3	Nuclear transcription factor	
		Subclass: aryl hydrocarbon receptor nuclear translocator; Arnt	
		Subclass: aryl hydrocarbon receptor nuclear translocator isoform 1; dioxin receptor, nuclear translocator; hypoxia-inducible factor 1, beta subunit	

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			Subclass: aryl-hydrocarbon receptor nuclear translocator 2; aryl hydrocarbon receptor nuclear translocator 2
			Subclass: BMAL1 protein (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (Basic-helix-loop-helix-PAS orphan MOP3) (BHLH-PAS protein JAP3).
			Subclass: brain and muscle Ah receptor nuclear translocator-like protein, BMAL1b
			Subclass: BMAL1c
5			Subclass: brain and muscle Ah receptor nuclear translocator-like protein, BMAL1d
			Subclass: brain and muscle Ah receptor nuclear translocator-like protein, BMAL1e
			Subclass: transcription factor BMAL2
			Subclass: brain-muscle-ARNT-like transcription factor 2a
			Subclass: brain-muscle-ARNT-like transcription factor 2b
10			Subclass: brain-muscle-ARNT-like transcription factor 2c
			Subclass: brain-muscle-ARNT-like transcription factor 2d
			Subclass: bHLH-PAS transcription factor MOP9
			Subclass: bHLH-PAS transcription factor MOP9
			Subclass: PAS protein 3
15			Subclass: cycle-like factor CLIF
	NM_013533		
20	NP_038561.1	F:(C-D)-2.1	protein 'A'
	1	3	Subclass: protein 'A' isoform 1; protein 'A'
			Subclass: protein 'A' isoform 2; protein 'A'
			Subclass: protein A-3
25	NM_013598		
	NP_038626.1	F:(C-D)-2.1	cell growth factor
	1	2	Subclass: mast cell growth factor

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			Subclass: mast cell growth factor, isoform b
			Subclass: stem cell growth factor
	NM_007753		Carboxypeptidase
5	NP_031779.1	F:(C-D)-2.0 8	
			Subclass: Carboxypeptidase A
			Subclass: Pancreatic carboxypeptidase A1
			Subclass: Carboxypeptidase A2
10			Subclass: carboxypeptidase A4; carboxypeptidase A3
			Subclass: carboxypeptidase A5
			Subclass: metallocarboxypeptidase A6
			Subclass: TPA: carboxypeptidase A-6; CPA6
15			Subclass: Mast cell carboxypeptidase A3 precursor
			Subclass: mast cell carboxypeptidase A; MC-CPA
			Subclass: carboxypeptidase B
			Subclass: plasma carboxypeptidase B2 isoform b; carboxypeptidase U; thrombin-activatable fibrinolysis inhibitor; carboxypeptidase B-like protein; thrombin-activatable fibrinolysis inhibitor
			Subclass: plasma carboxypeptidase B2 isoform a preproprotein; carboxypeptidase U; thrombin-activatable fibrinolysis inhibitor; carboxypeptidase B-like protein; thrombin-activatable fibrinolysis inhibitor
20			Subclass: carboxypeptidase O
			Subclass: TPA: carboxypeptidase O; CPO
	NM_019952		
25	NP_064336.1	F:(C-D)-2.0 7	cardiotrophin-like cytokine
			Subclass: cardiotrophin-like cytokine; neurotrophin-1/B-cell stimulating factor-3

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NM_025436				
NP_079712.1	F:(C-D)-2.0 4		sterol-C4-methyl oxidase-like; C-4 methyl sterol	
NM_019871				
NP_063924.1	F:(C-D)-2.0 4		condensing enzyme	
			Subclass: acyl-malonyl condensing enzyme	
			Subclass: hypothetical protein FLJ40154	
NM_009770				
NP_033900.1	F:(C-D)-2.0 2		B-cell translocation gene 3; abundant in neuroepithelium area	
NM_009993	F:(C-D) -3.27		cytochrome P450	
NP_034123.1			Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2; dioxin-inducible P3-450; P450 form 4; microsomal monooxygenase; xenobiotic monooxygenase; aryl hydrocarbon hydroxylase; flavoprotein-linked monooxygenase	
			Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase	
			Subclass: cytochrome P450 CYP1B1	
NM_007706	F:(C-D) -2.51		suppressor of cytokine signaling-2; STAT induced STAT inhibitor-2; cytokine-inducible SH2 protein 2	
NP_031732.1				
NM_009396	F:(C-D)-2.5		tumor necrosis factor, alpha-induced protein 2	
NP_033422.1				

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AK004924	F:(C-D)	similar to coenzyme A diphosphatase
BAB23675.1	-2.42	
NM_029813	F:(C-D) -2.4	zinc finger protein
NP_084089.1		
		Subclass: zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
		Subclass: similar to zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4
		Subclass: similar to zinc finger protein 91 (HPF7, HTF10)
		Subclass: zinc finger protein 180 (HHZ168)
		Subclass: zinc finger protein 136 (clone pHZ-20)
		Subclass: KIAA1710 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1710
		Subclass: Zinc finger protein 93 (Zinc finger protein HTF34)
		Subclass: zinc finger protein 135 (clone pHZ-17)
		Subclass: zinc finger protein 85 (HPF4, HTF1)
		Subclass: KIAA1198 protein
		Subclass: similar to Hypothetical zinc finger protein KIAA1198
		Subclass: similar to Zinc finger protein 135
		Subclass: similar to Zinc finger protein 93 (Zinc finger protein HTF34)
		Subclass: zinc finger protein 91 (HPF7, HTF10)
		Subclass: zinc finger protein 84 (HPF2)
		Subclass: finger protein 2, placental
		similar to KRAB zinc finger protein KR18
		Subclass: zinc finger protein AF020591
		Subclass: kruppel-related zinc finger protein
		Subclass: Similar to zinc finger protein 208
		Subclass: zinc finger protein 71; endothelial zinc finger protein induced by tumor necrosis factor alpha
		Subclass: zinc finger protein 37 homolog (mouse); Zinc finger protein-37, mouse, homolog of; zinc finger protein homologous to Zfp37 in mouse
		Subclass: zinc finger protein 328
		Subclass: similar to zinc finger protein 29

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	Subclass: zinc finger protein 268
	Similar to zinc finger protein 208
	Subclass: Zinc finger protein ZNF45
	Subclass: zinc finger protein 16 (KOX 9)
5	Subclass: similar to Zinc finger protein 85
	Subclass: zinc finger protein 43 (HTF6)
	Subclass: similar to Zinc finger protein 35 (Zfp-35)
	Subclass: zinc finger protein 228
	Subclass: similar to Zinc finger protein 20 (Zinc finger protein KOX13) (DKFZp572P0920)
	Subclass: similar to Zinc finger protein 184
10	Subclass: zinc finger protein 177
	Subclass: bB479F17.3 (zinc finger protein 41)
	Subclass: similar to Zinc finger protein 41
	Subclass: zinc finger protein 287
15	Subclass: zinc finger protein 331; zinc finger protein 463; C2H2-like zinc finger protein
	Subclass: zinc finger protein 271
	Subclass: Hypothetical zinc finger protein KIAA1473
	Subclass: similar to Hypothetical zinc finger protein KIAA1473
	Subclass: similar to Hypothetical zinc finger protein KIAA1956
20	Subclass: KRAB zinc finger protein
	Subclass: KIAA1956 protein
	Subclass: TRAF6-inhibitory zinc finger protein; TRAF6-binding zinc finger protein
	Alternate: hypothetical protein
	Subclass: FLJ40981
25	Subclass: similar to hypothetical protein FLJ40981
	Subclass: hypothetical protein FLJ21628
	Subclass: hypothetical protein FLJ32191
	Subclass: hypothetical protein DKFZp572C163.1
	Subclass: hypothetical protein FLJ30932
30	Subclass: hypothetical protein FLJ14345

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			Subclass: hypothetical protein FLJ90396
			Subclass: hypothetical protein FLJ31526
			Subclass: hypothetical protein DKFZp572P0920.1
5	NM_007494 NP_031520.1	F:(C-D) -2.36	argininosuccinate synthetase
			Subclass: argininosuccinate synthetase
			Subclass: similar to argininosuccinate synthetase
10	NM_008792 NP_032818.1	F:(C-D) -2.35	proprotein convertase subtilisin/kexin type 2; subtilisin-like prohormone convertases; prohormone convertase 2; neuroendocrine convertase 2; KEX2-like endoprotease 2; proprotein convertase PC5
	AK010786 BAB27182.1	F:(C-D) -2.27	tubulin, beta polypeptide
15			Subclass: tubulin, beta, 2
			Subclass: tubulin, beta, 4 (tubulin beta-III)
			Subclass: tubulin, beta, 5
			Subclass: tubulin beta-1
			Subclass: similar to tubulin, beta 3
20			Subclass: tubulin, beta polypeptide 4, member Q
			Subclass: beta tubulin 1, class VI
			Subclass: similar to beta-tubulin 4Q
			Alternative: similar to neu differentiation factor - human (fragment)
25	NM_008183 NP_032209.1	F:(C-D) -2.27	Glutathione S-transferase
			Subclass: similar to Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
			Subclass: glutathione transferase M1

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		Subclass: glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2
		Subclass: glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5
		Subclass: glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4
		Subclass: glutathione S-transferase M4 isoform 2; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4
5		Subclass: Similar to glutathione S-transferase M2 (muscle)
		Subclass: similar to Glutathione S-transferase Mu 3 (GSTM3-3) (GST class-mu 3) (hGSTM3-3)
		Subclass: Chain B, Ligand-Free Heterodimeric Human Glutathione S-Transferase M2-3 (Ec 2.5.1.18), Monoclinic Crystal Form
		Subclass: glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human
		Subclass: glutathione S-transferase M1 isoform 2; HB subunit 4; glutathione S-alkyltransferase; glutathione S-transferase, Mu-1; glutathione S-aryltransferase; S-(hydroxyalkyl)glutathione lyase; glutathione S-alkyltransferase; GST class-mu
10	NM_012006 NP_036136.1	F:(C-D) -2.24 Peroxisomal acyl-coenzyme A thioester hydrolase 2 (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128)
		Alternate: peroxisomal long-chain acyl-coA thioesterase; peroxisomal long-chain acyl-coA thioesterase ; putative protein
15	AK005569 BAB24656.1	F:(C-D) -2.18 hypothetical protein FLJ20456
		Alternate: Unknown (protein for MGC:21737)
20	NM_010107 NP_034237.1	F:(C-D) -2.18 ephraim-A1

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NM_025754	F:(C-D)	aldolase
NP_080030.1	-2.13	Subclass: Aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bisphosphatase
		Subclass: aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase
NM_008303	F:(C-D)	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (chaperonin 10)
NP_032329.1	-2.12	
NM_011300	F:(C-D)	ribosomal protein
NP_035430.1	-2.11	
		Subclass: ribosomal protein S7; 40S ribosomal protein S7
		Subclass: similar to ribosomal protein S7
AK011896	F:(C-D) -2.1	unnamed protein product
BAB27902.1		
NM_008322	F:(C-D) -2.1	isocitrate dehydrogenase 2 (NADP+), mitochondrial; Isocitrate dehydrogenase, mitochondrial
NP_032348.1		
NM_011802	F:(C-D)	ClpX caseinolytic protease X homolog; energy-dependent regulator of proteolysis; ClpX (caseinolytic protease X, E. coli)
NP_035932.1	-2.08	
AK004138	F:(C-D)	ORFII
BAB23187.1	-2.06	
		Alternative: hypothetical protein FLJ20048
		Alternative: putative p150
NM_008509	F:(C-D)	lipoprotein lipase
NP_032535.1	-2.05, F:(HI-D)	
	-2.42	

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			Subclass: lipoprotein lipase precursor
			Subclass: Similar to lipoprotein lipase
			Subclass: lipoprotein lipase
5	NM_013541	F:(C-D)	glutathione S-transferase
	NP_038569.1	-2.05	
			Subclass: glutathione transferase pi
			Subclass: glutathione S-transferase-P1c
			Subclass: Chain A, Glutathione S-Transferase P1-1
10			Subclass: glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester synthase III
	NM_008756	F:(C-D)	occludin
	NP_032782.1	-2.04	
15	NM_009349	F:(C-D)	Methyltransferase
	NP_033375.1	-2.04	
			Subclass: Indolethylamine N-methyltransferase (Aromatic alkylamine N-methyltransferase) (Indolamine N-methyltransferase) (Arylamine N-methyltransferase) (Amine N-methyltransferase)
			Subclass: indolethylamine N-methyltransferase; thioester S-methyltransferase-like
			Subclass: thioether S-methyltransferase-like; similar to P40936 (PID:g731019)
20			Subclass: nicotinamide N-methyltransferase
	NM_023850	F:(C-D)	carbohydrate sulfotransferase
	NP_076339.1	-2.03	
			Subclass: carbohydrate (keratan sulfate Gal-6) sulfotransferase 1; carbohydrate (chondroitin 6/keratan) sulfotransferase 1
			Subclass: carbohydrate (chondroitin 6) sulfotransferase 3; chondroitin 6-sulfotransferase
25			Subclass: carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6; macular dystrophy, corneal, 1; carbohydrate sulfotransferase 6; corneal N-acetylglucosamine 6-sulfotransferase
			Subclass: carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4; N-acetylglucosamine 6-O-sulfotransferase

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NM_033146	F:(C-D)	Protein CGI-112
NP_149158.1	-2.03	
		Alternate: similar to Protein CGI-112
NM_010324	F:(C-D)	aspartate aminotransferase
NP_034454.1	-2.01	
		Subclass: aspartate aminotransferase 1; glutamic-oxaloacetic transaminase 1, soluble
		Subclass: glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
NM_016978	F:(C-D)	Ornithine aminotransferase
NP_058674.1	-2.01	
NM_011172	F:(C-D) -2	proline dehydrogenase (oxidase) 1; proline oxidase 2; p53 induced protein
NP_035302.1		
NM_013809	F:(C-D) -2	cytochrome P450
NP_038837.1		
		Subclass: Cytochrome P450 2A13 (CYP1A13)
		Subclass: coumarin 7-hydroxylase (EC 1.14.14.-) cytochrome P450 2A6 -
		Subclass: Cytochrome P450 2A7 (CYP1A7) (P450-IIA4)
		Subclass: cytochrome P450 2A4 - human
		Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
		Subclass: cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; similar to cytochrome P450, subfamily IIF, polypeptide 1 (H. sapiens)
		Subclass: cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYP1C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)

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		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYP1C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
		Subclass: cytochrome P450, subfamily IIE, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)
		Subclass: cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P450, subfamily IIS, polypeptide 1
		Subclass: cytochrome P450, subfamily IIJ (arachidonic acid epoxidase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase; Cytochrome P450, subfamily IIJ (arachidonic acid epoxidase),
		Subclass: cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C17
		Subclass: Cytochrome P450 2C18 (CYP1C18) (P450-6B/29C)
		glutathione transferase
NM_008184	F:(C-D)	
NP_032210.1	-1.78	
		Subclass: Glutathione S-transferase Mu 1 (GSTM1-1) (HB subunit 4) (GTH4) (GSTM1a-1a) (GSTM1b-1b) (GST class-mu 1)
		Subclass: glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle; GST class-mu 2; glutathione S-transferase Mu 2; glutathione S-alkyltransferase M2; glutathione S-aryltransferase M2; S-(hydroxyalkyl)glutathione lyase M2; glutathione S-alkyltransferase M2
		Subclass: glutathione S-transferase M4 isoform 1; glutathione S-transferase, Mu-4; glutathione S-alkyltransferase M4; glutathione S-aryltransferase M4; S-(hydroxyalkyl)glutathione lyase M4; glutathione S-alkyltransferase M4; GTS-Mu2; GST class-mu 4
		Subclass: glutathione S-transferase M5; glutathione S-transferase, Mu-5; glutathione S-alkyltransferase M5; glutathione S-aryltransferase M5; S-(hydroxyalkyl)glutathione lyase M5; glutathione S-alkyltransferase M5; GST class-mu 5
		Subclass: glutathione transferase (EC 2.5.1.18) class mu, GSTM3 - human
AK003797	F:(C-D)	molybdenum cofactor sulfurase
BAB23001.1	-1.71	
		Alternate: Similar to molybdenum cofactor sulfurase

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S80191	F:(C-D)	Unknown (protein for MGC:9220)
AAB21335.1	-1.61	Alternate: carboxylesterase
		Subclass: carboxylesterase 1 (monocyte/macrophage serine esterase 1); liver carboxylesterase; carboxylesterase 2 (liver)
		Subclass: acyl coenzyme A:cholesterol acyltransferase
		Subclass: brain carboxylesterase hBr1
		Subclass: brain carboxylesterase hBr2
		Subclass: egasyn
		Subclass: Liver carboxylesterase precursor (Acyl coenzyme A:cholesterol acyltransferase) (ACAT) (Monocyte/macrophage serine esterase) (HMSE) (Serine esterase 1) (Brain carboxylesterase hBr1)
		Subclass: carboxylesterase 3; brain carboxylesterase BR3
		Subclass: serine esterase N-terminal truncated (503 AA)
		Subclass: carboxylesterase 2; intestinal carboxylesterase; liver carboxylesterase-2
		Subclass: Similar to carboxylesterase 2 (intestine, liver)
AK014166	F:(C-D)	Delta(14)-sterol reductase (C-14 sterol reductase) (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1)
BAB29187.1	-1.58	Alternate: Similar to transmembrane 7 superfamily member 2
		Alternate: lamin B receptor
		Alternate: similar to Lamin B receptor (Integral nuclear envelope inner membrane protein) (LMN2R)
		Alternate: integral nuclear envelope inner membrane protein

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Master Table 2: Subtable 2B Classes of Unfavorable Genes/Proteins

Main	Behavior	Human Protein Name
NM_033373	U:(C-D)	Keratin
NP_203537.1	+7.74	
		Subclass: Keratin, type I cytoskeletal
		Subclass: Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23).
		Subclass: Keratin 23 isoform a; histone deacetylase inducible keratin 23; hyperacetylation-inducible type I keratin; keratin, type I cytoskeletal 23; cytokeratin 23; type I intermediate filament
		cytokeratin
		Subclass: keratin 23 isoform b; histone deacetylase inducible keratin 23; hyperacetylation-inducible type I keratin; keratin, type I cytoskeletal 23; cytokeratin 23; type I intermediate filament cytokeratin
		Subclass: cytokeratin 9
		Subclass: Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
		Subclass: keratin 12 (Meesmann corneal dystrophy); Keratin-12; keratin 12
		Subclass: keratin 13 isoform a; keratin, type I cytoskeletal 13; cytokeratin 13
		Subclass: keratin 13 isoform b; keratin, type I cytoskeletal 13; cytokeratin 13
		Subclass: keratin 14, type I, cytoskeletal
		Subclass: keratin 15; keratin-15, basic; keratin-15, beta; type I cytoskeletal 15; cytokeratin 15, (Cytokeratin 15) (K15) (CK 15)
		Subclass: keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16
		Subclass: keratin 17
		Subclass: cytokeratin 18
		Subclass: Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19), 40-kd; cytokeratin 19; 40-kDa keratin intermediate filament precursor gene
		Subclass: keratin 20; cytokeratin 20; keratin, type I cytoskeletal 20
		Subclass: keratin 24
		Subclass: Keratin, type I cuticular HA1 (Hair keratin, type I HA1).
		Subclass: type I hair keratin 2; Ha-2; hard keratin, type I, 2; keratin, hair, acidic, 2

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			Subclass: type I hair keratin 3A; Ha-3I; hard keratin, type I,3I; keratin, hair, acidic,3A
			Subclass: type I hair keratin 3B; Ha-3II; hard keratin, type I, 3II; keratin, hair, acidic,3B
			Subclass: Keratin, type I cuticular HA4 (Hair keratin, type I HA4).
			Subclass: type I hair keratin 5; Ha-5; hard keratin, type I, 5
			Subclass: type I hair keratin 6
			Subclass: type I hair keratin 7
			Subclass: Keratin, type I cuticular HA8 (Hair keratin, type I HA8).
			Subclass: type I intermediate filament cytokeratin
	NM_007702	U:(C-D)	cell death activator CIDE-A
10	NP_031728.1	+4.7	Alternate: Similar to cell death-inducing DFFA-like effector a
	AK013885	U:(C-D)	BRCA1 associated protein
	NP_082503.1	+4.18	
			Subclass: BRCA1-associated protein 2
15			Subclass: putative DDB p127-associated protein
	NM_011995	U:(C-D)	
	NP_036125.2	+4.17	presynaptic cytomatrix protein
			Subclass: Piccolo protein (Aczonin).
20			Alternate: Zinc finger protein
	NM_013623	U:(C-D)	
	NP_038651.1	+4.05	Glycoprotein
			Subclass: Orosomucoid-1 (alpha-1-acid glycoprotein-1); alpha-1-acid glycoprotein 1
25			Subclass: orosomucoid 2; alpha-1-acid glycoprotein, type 2
	NM_008484	U:(C-D)	
	NP_032510.1	+4.05	Laminin
30			Subclass: Laminin beta chain

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		Subclass: laminin, beta 1	
		Subclass: beta2/S laminin chain	
		Subclass: Laminin beta-2 chain (S-laminin) (Laminin B1s chain).	
		Subclass: Laminin beta-3 chain (Laminin 5 beta 3) (Laminin B1k chain) (Kalinin B1 chain).	
		Subclass: laminin S B3 chain	
		Subclass: Laminin alpha chain	
		Subclass: Laminin alpha-1 chain precursor (Laminin A chain).	
		Subclass: laminin alpha 3b chain	
		Subclass: laminin alpha 5; laminin alpha-5 chain	
		Subclass: Laminin gamma chain	
		Subclass: Laminin gamma-3 chain (Laminin 12 gamma 3).	
		Alternate: Usher syndrome type IIa protein	
		Alternate: netrin	
		Subclass: netrin 4; beta-netrin	
		Subclass: netrin 1; netrin 1, mouse, homolog of	
NM_013786	U:(C-D)	sterol/retinol dehydrogenase	
NP_038814.1	+3.68		
		Subclass: 3-hydroxysteroid epimerase; oxidative 3-alpha-hydroxysteroid-dehydrogenase; 3(alpha->beta)-hydroxysteroid epimerase; retinol dehydrogenase; oxidoreductase; NAD+ -dependent 3 alpha-hydroxysteroid dehydrogenase	
		Subclass: microsomal NAD+-dependent retinol dehydrogenase 4	
		Subclass: orphan short-chain dehydrogenase / reductase; retinol dehydrogenase similar protein	
		Subclass: 11-cis retinol dehydrogenase (11-cis RDH).	
		Subclass: retinol dehydrogenase 5 (11-cis and 9-cis); retinol dehydrogenase 5 (11-cis and 9-cis)	
		Subclass: retinol dehydrogenase homolog isoform-1	
NM_009345	U:(C-D)		
NP_033371.1	+3.66	DNA synthesizing/modifying enzymes	
		Subclass: DNA nucleotidylexotransferase (Terminal addition enzyme) (Terminal deoxynucleotidyltransferase) (Terminal transferase).	
		Subclass: polymerase (DNA directed), mu; polymerase (DNA-directed), mu; pol iota	

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NM_013703	U:(C-D)	Lipoprotein Receptor	
NP_038731.1	+3.61		
		Subclass: very low density lipoprotein receptor	
		Subclass: low density lipoprotein receptor ; LDL receptor; LDLR precursor	
		Subclass: apolipoprotein E receptor 2 isoform 1 precursor; apolipoprotein E receptor 2	
		Subclass: apolipoprotein E receptor 2 isoform 2 precursor; apolipoprotein E receptor 2	
		Subclass: apolipoprotein E receptor 2 isoform 3 precursor; apolipoprotein E receptor 2	
		Subclass: low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	
		Subclass: low density lipoprotein-related protein 2; megalin	
		Subclass: low density lipoprotein receptor related protein 1B (deleted in tumors); low density lipoprotein receptor related protein-deleted in tumor	
		Subclass: LDL receptor member LR3	
		Subclass: low density lipoprotein receptor-related protein 5; low density lipoprotein receptor-related protein 7; osteoporosis pseudoglioma syndrome	
		Subclass: low density lipoprotein receptor-related protein 6; low density lipoprotein-related protein 6	
		Subclass: apolipoprotein E receptor 2 906	
		Subclass: glycoprotein 330	
		Subclass: MEGF7	
		Subclass: similar to MEGF7	
NM_022414	U:(C-D)		
NP_071859.1	+3.28	oxygen-binding respiratory protein	
		Subclass: neuroglobin	
NM_011313	U:(C-D)		
NP_035443.1	+2.77	Calcium-binding protein	
		Subclass: S100 calcium-binding protein A6; calyculin; prolactin receptor-associated protein	

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AK005519 I49390	U:(C-D) +2.7	
	U:(C-HI))+2.7	Major epididymis-specific protein E4 precursor (HE4) (Epididymal secretory protein E4) (WAP four-disulfide core domain protein 2)
NM_008745	U:(C-D) +2.68	
NP_032771.1		Tyrosine Kinase Receptor
		Subclass: brain-derived neurotrophic factor receptor precursor, short splice form
		Subclass: neurotrophic tyrosine kinase, receptor, type 2
		Subclass: BDNF/NT-3 growth factors receptor precursor (TrkB tyrosine kinase) (GP145-TrkB) (Trk-B).
		Subclass: NT-3 growth factor receptor precursor (TrkC tyrosine kinase) (GP145-TrkC) (Trk-C)
		Subclass: neurotrophic tyrosine kinase, receptor, type 3
		Subclass: neurotrophic tyrosine kinase, receptor, type 1; Oncogene TRK
NM_008063	U:(C-D) +2.68	
NP_032089.1		glucose-6-phosphate transporter
		Subclass: glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1; Glucose-6-phosphate transporter-1
NM_019696	U:(C-D) +2.66	
NP_062670.1		carboxypeptidase
		Subclass: adipocyte enhancer binding protein 1 precursor; AE-binding protein 1; adipocyte transcription factor, AEBP1; aortic carboxypeptidase-like protein
		Subclass: metalloproteinase CPX-1 precursor
		Subclass: Potential carboxypeptidase X precursor (Metalloproteinase CPX-1).
		Subclass: carboxypeptidase D
		Subclass: carboxypeptidase E
		Subclass: carboxypeptidase M
		Subclass: carboxypeptidase N, polypeptide 1
		Subclass: Similar to carboxypeptidase X (M14 family)

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			Subclass: Similar to carboxypeptidase Z
			Subclass: similar to Potential carboxypeptidase-like protein X2 precursor
			Subclass: Potential carboxypeptidase-like protein X2 precursor
NM_053261	U:(C-D)		inositol monophosphatase
NP_444491.1	+2.63		Subclass: inositol(myo)-1(or 4)-monophosphatase 1
			Subclass: inositol(myo)-1(or 4)-monophosphatase 2
			Subclass: brain myo-inositol monophosphatase A2b; IMPase A2b
			Subclass: Chain A, Human Inositol Monophosphatase (E.C.3.1.3.25) Dimer Complex With Gadolinium And Sulfate
NM_008218	U:(C-D)		Hemoglobin
NP_032244.1	+2.6		Subclass: hemoglobin alpha-1 globin chain
			Subclass: hemoglobin alpha-2
NM_018887	U:(C-D)		Cytochrome P450
NP_061375.1	+2.54		Subclass: cytochrome P450, family 39, subfamily A, polypeptide 1; oxysterol 7alpha-hydroxylase; cytochrome P450, subfamily XXXIX (oxysterol 7 alpha-hydroxylase), polypeptide 1
NM_009148	U:(C-D)		Exocyst complex component
NP_033174.1	+2.45		Subclass: Exocyst complex component Sec8
NM_013790	U:(C-D)		Multidrug resistance-associated protein (Multi-specific organic anion transporter; ATP-binding cassette
NP_038818.1	+2.45		Subclass: Multidrug resistance-associated protein 5 (Multi-specific organic anion transporter-C) (MOAT-C) (pABC11) (SMRP).
			Subclass: ATP-binding cassette, sub-family C, member 5; canalicular multispecific organic anion transporter C
			Subclass: ATP-binding cassette protein C11

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	Subclass: ATP-binding cassette, sub-family C, member 11 isoform a; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11
	Subclass: ATP-binding cassette, sub-family C, member 11 isoform b; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11
	Subclass: ATP-binding cassette, sub-family C, member 12 isoform a; multidrug resistance-associated protein 9
	Subclass: ATP-binding cassette, sub-family C, member 12 isoform b; multidrug resistance-associated protein 9
	Subclass: ATP-binding cassette, sub-family C, member 12 isoform e; multidrug resistance-associated protein 9
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 1; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 2; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 3; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 4; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 5; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 6; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C, member 1 isoform 7; multiple drug resistance-associated protein; multiple drug resistance protein 1; multidrug resistance protein
	Subclass: ATP-binding cassette, sub-family C (CFTR/MRP), member 2; canalicular multispecific organic anion transporter
	Subclass: ATP-binding cassette, sub-family C, member 9 isoform SUR2B; sulfonyleurea receptor 2A
	Subclass: ATP-binding cassette, sub-family C, member 3 isoform MRP3A; canalicular multispecific organic anion transporter
	Subclass: ATP-binding cassette, sub-family C, member 4; canalicular multispecific organic anion transporter (ABC superfamily)
	Subclass: ATP-binding cassette, subfamily B, member 4 isoform A; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3
	Subclass: ATP-binding cassette, subfamily B, member 4 isoform B; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3

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		Subclass: ATP-binding cassette, subfamily B, member 4 isoform C; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3
		Subclass: ATP-binding cassette, sub-family C, member 6; anthracycline resistance-associated
		Subclass: cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7); cystic fibrosis transmembrane conductance regulator; ATP-binding cassette, sub-family C member 7; CFTR/MRP
		Subclass: ATP-binding cassette, sub-family C, member 8; Sulfonylurea receptor; sulfonylurea receptor (hyperinsulinemia)
		Subclass: ATP-binding cassette, sub-family C, member 9 isoform SUR2A-delta-14; sulfonylurea receptor 2A
		Subclass: ATP-binding cassette, sub-family C, member 10; multidrug resistance-associated protein 7
		Subclass: ATP-binding cassette, sub-family B (MDR/TAP), member 1; P glycoprotein 1/multiple drug resistance 1; P-glycoprotein-1/multiple drug resistance-1; multidrug resistance 1
		Subclass: Cystic fibrosis transmembrane conductance regulator (CFTR) (cAMP-dependent chloride channel).
NM_008532	U:(C-D)	Membrane glycoprotein
NP_032558.1	+2.41	Subclass: Cell-surface receptor
		Subclass: Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated antigen) (KSA) (KS 1/4 antigen) (Cell surface glycoprotein Trop-1).
		Subclass: tumor-associated calcium signal transducer 1 precursor; membrane component, chromosome 4, surface marker (35kD glycoprotein); MK-1 antigen; antigen identified by monoclonal antibody AUA1
		Subclass: tumor-associated calcium signal transducer 2 precursor; membrane component, chromosome 1, surface marker 1 (40kD glycoprotein identified by monoclonal antibody GA733); epithelial glycoprotein-1
		Subclass: Tumor-associated calcium signal transducer 2 precursor (Pancreatic carcinoma marker protein GA733-1) (Cell surface glycoprotein Trop-2).
NM_013722	U:(C-D)	Regulator of neurotransmitter release
NP_038750.1	+2.35	Subclass: Synapsins
		Subclass: Synapsin III
		Subclass: synapsin III isoform IIIa

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			Subclass: synapsin III isoform IIIc
			Subclass: synapsin III isoform IIIb
			Subclass: Synapsin II
			Subclass: synapsin II isoform IIa
			Subclass: synapsin II isoform IIb
			Subclass: Synapsin I (Brain protein 4.1).
			Subclass: synapsin I isoform Ia; brain protein 4.1
			Subclass: synapsin I isoform Ib; brain protein 4.1
NM_008439	U:(C-D)		
NP_032465.1	+2.35		Fructose metabolizing enzymes
			Subclass: ketohexokinase
			Subclass: ketohexokinase isoform a
			Subclass: ketohexokinase isoform b
NM_007408	U:(C-D)		
NP_031434.1	+2.35		Lipid storage proteins
			Subclass: Adipophilin (Adipose differentiation-related protein) (ADRP).
			Subclass: Cargo selection protein TTP47 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Placental protein 17).
NM_011200	U:(C-D)		
NP_035330.1	+2.3		protein tyrosine phosphatase
			Subclass: protein tyrosine phosphatase type IV
			Subclass: protein tyrosine phosphatase type IVA, member 1; Protein tyrosine phosphatase IVA1
			Subclass: protein tyrosine phosphatase type IVA, member 2 isoform 1; protein tyrosine phosphatase IVA2; protein tyrosine phosphatase IVA;
			phosphatase of regenerating liver 2
			Subclass: ptp-IV1b, PTP-IV1 gene product
			Subclass: protein tyrosine phosphatase type IVA, member 3 isoform 1; potentially prenylated protein tyrosine phosphatase
			Subclass: protein tyrosine phosphatase type IVA, member 3 isoform 2; potentially prenylated protein tyrosine phosphatase

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NM_007405	U:(C-D)	Adenylate cyclase
NP_031431.1	+2.29	Subclass: Adenylate cyclase, type I (ATP pyrophosphate-lyase) (Ca(2+)/calmodulin activated adenylate cyclase).
		Subclass: adenylate cyclase 2; ATP pyrophosphate-lyase; type II adenylate cyclase; adenylate cyclase 2; adenylate cyclase II; 3',5'-cyclic AMP synthetase
		Subclass: adenylate cyclase 3; adenylate cyclase, type III; ATP pyrophosphate-lyase
		Subclass: adenylate cyclase 4; adenylate cyclase type IV
		Subclass: Adenylate cyclase, type V (ATP pyrophosphate-lyase) (Adenylate cyclase).
		Subclass: adenylate cyclase type VI
		Subclass: adenylate cyclase 6 isoform a
		Subclass: adenylate cyclase 6 isoform b
		Subclass: adenylate cyclase 7
		Subclass: adenylate cyclase 8; Adenylate cyclase-8, brain
		Subclass: Adenylate cyclase, type IX (ATP pyrophosphate-lyase) (Adenylate cyclase).
AK007384	U:(C-D)	sulfotransferase
BAB25002.1	+2.27	Subclass: sulfotransferase family, cytosolic, 1C, member 1 isoform a; sulfotransferase 1C1
		Subclass: sulfotransferase family, cytosolic, 1C, member 2; sulfotransferase family, cytosolic, 1C, member C2; sulfotransferase 1C2
		Subclass: Phenol-sulfating phenol sulfotransferase 1 (P-PST) (Thermostable phenol sulfotransferase) (Ts-PST) (HAST1/HAST2) (ST1A3).
		Subclass: sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; thermostable phenol sulfotransferase; phenolic-metabolizing (P) form of PST; arylamine sulfotransferase; aryl sulfotransferase; phenol-preferring phenol sulfotransferase2; phenol-sulfating phenol sulfotransferase 2
		Subclass: sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; thermolabile phenol sulfotransferase; catecholamine-sulfating phenol sulfotransferase; aryl sulfotransferase; thermolabile (monoamine, M form) phenol sulfotransferase; monoamine-sulfating phenosulfotransferase; placental estrogen sulfotransferase; monoamine-preferring sulfotransferase
		Subclass: Alcohol sulfotransferase (Hydroxysteroid Sulfotransferase) (HST) (Dehydroepiandrosterone sulfotransferase) (DHEA-ST) (ST2) (ST2A3).
		Subclass: hydroxysteroid sulfotransferase SUL2B1a

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			Subclass: hydroxysteroid sulfotransferase SULT2B1b
			Subclass: thyroid hormone sulfotransferase
	NM_013738	U:(C-D)	
5	NP_038766.1	+2.25	Pleckstrin
			Subclass: pleckstrin; p47
			Subclass: pleckstrin 2; pleckstrin 2 (mouse) homolog
	NM_013757	U:(C-D)	
10	NP_038785.1	+2.22	synaptotagmin-like proteins
			Subclass: synaptotagmin-like 4 (granuphilin-a)
			Subclass: bA524D16A.2.1 (novel protein similar to mouse granuphilin-a)
			Subclass: bA524D16A.2.2 (novel protein similar to mouse granuphilin-b)
			Subclass: synaptotagmin-like 5
15			Subclass: synaptotagmin-like 2 isoform b; chromosome 11 synaptotagmin
			Subclass: synaptotagmin-like 2 isoform a; chromosome 11 synaptotagmin
	NM_009368	U:(C-D)	
	NP_033394.1	+2.22	Growth factor
			Subclass: Transforming growth factor
20			Subclass: Transforming growth factor beta
			Subclass: Transforming growth factor beta 1 (TGF-beta 1).
			Subclass: transforming growth factor beta 2
			Subclass: transforming growth factor-beta 3
25	NM_013750	U:(C-D)	
	NP_038778.1	+2.21	Protein containing pleckstrin homology-like domain
			Subclass: pleckstrin homology-like domain, family A, member 3; pleckstrin homology-like domain, family A, member 2

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NM_008471	U:(C-D)	Keratin
NP_032497.1	+2.21	
		Subclass: cytokeratin 9
		Subclass: Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
		Subclass: Keratin-12
		Subclass: keratin 13, type I, cytoskeletal
		Subclass: keratin 14, type I, cytoskeletal
		Subclass: keratin 15, basic; keratin-15, beta; type I cytoskeletal 15; cytokeratin 15
		Subclass: keratin 16, type I, cytoskeletal
		Subclass: keratin 17
		Subclass: keratin 18
		Subclass: keratin 19; keratin, type I cytoskeletal 19; keratin, type I, 40-kd; cytokeratin 19; 40-kDa keratin intermediate filament precursor gene
		Subclass: keratin 20; cytokeratin 20; keratin, type I cytoskeletal 20
		Subclass: Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23).
		Subclass: keratin 24
		Subclass: type I hair keratin 1; Ha-1; hard keratin, type I, 1; keratin, hair, acidic, 1
		Subclass: type I hair keratin 2; Ha-2; hard keratin, type I, 2; keratin, hair, acidic, 2
		Subclass: Keratin, type I cuticular HA3-I (Hair keratin, type I HA3-I).
		Subclass: type I hair keratin 3A; Ha-3I; hard keratin, type I, 3I; keratin, hair, acidic, 3A
		Subclass: type I hair keratin 3B; Ha-3II; hard keratin, type I, 3II; keratin, hair, acidic, 3B
		Subclass: hair keratin acidic 3-II
		Subclass: Keratin, type I cuticular HA4 (Hair keratin, type I HA4).
		Subclass: Keratin, type I cuticular HA5 (Hair keratin, type I HA5).
		Subclass: type I hair keratin 6
		Subclass: type I hair keratin 7
		Subclass: type I hair keratin 8
NM_010707	U:(C-D)	
NP_034837.1	+2.2	galectin
		Subclass: galectin 4; lectin galactoside-binding soluble 4

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NM_010003	U:(C-D)	cytochrome P450
NP_034133.1	+2.18	Subclass: cytochrome P450, family 2
		Subclass: cytochrome P450, family 2, subfamily C
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 19; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450 arachidonic acid epoxidase isoform, Cyp 2C8 [human, kidney, Peptide Partial, 485 aa]
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 8 isoform 1; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form I
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 8 isoform 2; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; P450 form I
		Subclass: cytochrome P450, family 2, subfamily C, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 9
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)
		Subclass: cytochrome P450, family 2, subfamily A
		Subclass: cytochrome P450, family 2, subfamily A, polypeptide 6; coumarin 7-hydroxylase; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 3; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, family 2, subfamily A, polypeptide 7 isoform 1; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7
		Subclass: cytochrome P450, family 2, subfamily A, polypeptide 13; cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 13
		Subclass: cytochrome P450, family 2, subfamily B
		Subclass: cytochrome P450, family 2, subfamily B, polypeptide 6; cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6

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		Subclass: cytochrome P450, subfamily IID
		Subclass: cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase;
		flavoprotein-linked monooxygenase; cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing)-like 1
		Subclass: cytochrome P450, family 2, subfamily E
		Subclass: cytochrome P450, family 2, subfamily E, polypeptide 1; cytochrome P450, subfamily IIE (ethanol-inducible), polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase; cytochrome P450, subfamily IIE (ethanol-inducible)
		Subclass: cytochrome P450, family 2, subfamily F
		Subclass: cytochrome P450, family 2, subfamily F, polypeptide 1; cytochrome P450, subfamily IIF, polypeptide 1; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, family 2, subfamily J
		Subclass: cytochrome P450, family 2, subfamily J, polypeptide 2; cytochrome P450, subfamily IJJ (arachidonic acid epoxidase) polypeptide 2; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, family 2, subfamily S
		Subclass: cytochrome P450, family 2, subfamily S, polypeptide 1; cytochrome P450 family member predicted from ESTs; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide 1
		Subclass: cytochrome P450, family 1
		Subclass: cytochrome P450, family 1, subfamily A
		Subclass: cytochrome P450, family 1, subfamily A, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase
		Subclass: cytochrome P450, family 1, subfamily B
		Subclass: cytochrome P450, family 1, subfamily B, polypeptide 1; aryl hydrocarbon hydroxylase; cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile); microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
NM_019875	U:(C-D)	ABC-transporter; peptide transporter; ATP-binding cassette
NP_063928.1	+2.17	
		Subclass: ATP-binding cassette, sub-family B, member 9 isoform 1

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		Subclass: ATP-binding cassette, sub-family B, member 9 isoform 2
		Subclass: transporter 2, ATP-binding cassette, sub-family B isoform 1; transporter 2, ABC (ATP binding cassette); ATP-binding cassette, sub-family B (MDR/TAP), member 3; antigen peptide transporter 2; peptide supply factor 2; peptide transporter PSF2; ABC transporter, MHC 2
		Subclass: transporter 1, ATP-binding cassette, sub-family B; ATP-binding cassette, sub-family B (MDR/TAP), member 2; antigen peptide transporter 1; ATP-binding cassette, sub-family B, member 2; transporter, ATP-binding cassette, major histocompatibility complex, 1; ABC transporter, MHC 1; peptide supply factor 1
		Subclass: Antigen peptide transporter 1 (APT1) (Peptide transporter TAP1) (Peptide transporter PSF1) (Peptide supply factor 1) (PSF-1) (Peptide transporter involved in antigen processing 1).
		Subclass: Antigen peptide transporter 2 (APT2) (Peptide transporter TAP2) (Peptide transporter PSF2) (Peptide supply factor 2) (PSF-2)(Peptide transporter involved in antigen processing 2).
		Subclass: transporter 2, ATP-binding cassette, sub-family B isoform 2; transporter 2, ABC (ATP binding cassette); ATP-binding cassette, sub-family B (MDR/TAP), member 3; antigen peptide transporter 2; peptide supply factor 2; peptide transporter PSF2; ABC transporter, MHC 2
		Subclass: ATP-binding cassette, subfamily B, member 4 isoform A; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3
		Subclass: ATP-binding cassette, subfamily B, member 4 isoform B; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3
		Subclass: ATP-binding cassette, subfamily B, member 4 isoform C; P glycoprotein 3/multiple drug resistance 3; P-glycoprotein-3/multiple drug resistance-3; multiple drug resistance 3
		Subclass: ATP-binding cassette, sub-family B, member 6
		Subclass: ATP-binding cassette, sub-family B, member 7, mitochondrial precursor (ATP-binding cassette transporter 7) (ABC transporter 7 protein).
		Subclass: ATP-binding cassette, sub-family B, member 8, mitochondrial precursor (Mitochondrial ATP-binding cassette 1) (M-ABC1).
		Subclass: ATP-binding cassette, sub-family B, member 10
		Subclass: ATP-binding cassette, sub-family B (MDR/TAP), member 11; ABC member16, MDR/TAP subfamily; progressive familial intrahepatic cholestasis 2; bile salt export pump
NM_007471	U:(C-D)	amyloid protein
NP_031497.1	+2.16	

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			Subclass: amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease); Amyloid beta (A4) precursor protein; amyloid beta-peptide
			Subclass: amyloid precursor protein homolog HSD-2
			Subclass: amyloid A4 protein
5	AF232828	U:(C-D) +2.15	neuro-oncological ventral antigen
	AAF35907.1		Subclass: neuro-oncological ventral antigen 1 isoform 1; Neurooncological ventral antigen 1; paraneoplastic Ri antigen
			Subclass: neuro-oncological ventral antigen 1 isoform 2; Neurooncological ventral antigen 1; paraneoplastic Ri antigen
			Subclass: neuro-oncological ventral antigen 2; neuro-oncological ventral antigen 3
10			Subclass: astrocytic NOVA-like RNA-binding protein
			Subclass: RNA-binding protein Nova-2 [AA 29-492]; astrocytic NOVA-like RNA-binding protein
	NM_008212	U:(C-D) +2.15	3-hydroxyacyl-CoA dehydrogenase
	NP_032238.1		Subclass: Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor (HCDH) (Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase).
15			Subclass: 3-hydroxyacyl-CoA dehydrogenase, isoform 2
			Down syndrome critical protein
	NM_007834	U:(C-D) +2.14	Down syndrome critical protein
	NP_031860.1		Subclass: Down syndrome critical region protein 3; Down syndrome critical region protein A
20			Subclass: Down syndrome critical protein A - human
	NM_008030	U:(C-D) +2.14	monooxygenase
	NP_032056.1		Subclass: Flavin containing monooxygenase
25			Subclass: flavin containing monooxygenase 1; Flavin-containing monooxygenase 1 (fetal liver)
			Subclass: flavin containing monooxygenase 2; Flavin-containing monooxygenase 2 (adult liver)

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		Subclass: Dimethylaniline monooxygenase [N-oxide forming] 2 (Pulmonary flavin-containing monooxygenase 2) (FMO 2) (Dimethylaniline oxidase 2) (FMO 1B1).
		Subclass: Flavin containing monooxygenase 3
		Subclass: Dimethylaniline monooxygenase [N-oxide forming] 3 (Hepatic flavin-containing monooxygenase 3) (FMO 3) (Dimethylaniline oxidase 3) (FMO form 2) (FMO II).
		Subclass: flavin containing monooxygenase 4
5		Subclass: flavin containing monooxygenase 5
		Subclass: Dimethylaniline monooxygenase [N-oxide forming] 5 (Hepatic flavin-containing monooxygenase 5) (FMO 5) (Dimethylaniline oxidase 5).
		Subclass: dimethylaniline monooxygenase [N-oxide forming] 6 (Flavin-containing monooxygenase 6) (FMO 6) (Dimethylaniline oxidase 6).
10	NM_009073 NP_033099.1	U:(C-D) +2.13 retinal outer segment membrane protein _
		Subclass: retinal outer segment membrane protein 1; rod outer segment membrane protein 1
	NM_020568 NP_065593.1	U:(C-D) +2.12 KIAA1881 protein
15	NM_033327 NP_201584.1	U:(C-D) +2.12 zinc finger protein
		Subclass: OLF-1/EBF associated zinc finger protein; Smad- and Olf-interacting zinc finger protein
		Subclass: early hematopoietic zinc finger
		Subclass: FLJ00107 protein
20		Subclass: zinc finger protein 91 (HPF7, HTF10)
		Subclass: zinc finger protein 208
	NM_010902 NP_035032.1	U:(C-D) +2.11 Nuclear transcription factor
25		Subclass: transcription factor Nrf1
		Subclass: transcription factor Nrf2
		Subclass: nuclear factor (erythroid-derived 2)-like 1; transcription factor 11 (basic leucine zipper type)

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			Subclass: nuclear factor (erythroid-derived 2)-like 2 Subclass: transcription factor LCR-F1.
5	NM_010217 NP_034347.1	U:(C-D) +2.1	growth factor Subclass: connective tissue growth factor Subclass: CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (IGF1 protein). Subclass: WNT1 inducible signaling pathway protein 1 isoform 1 precursor; wnt-1 signaling pathway protein 1; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1 Subclass: WNT1 inducible signaling pathway protein 2 precursor; wnt-1 signaling pathway protein 2; connective tissue growth factor-like protein Subclass: WNT1 inducible signaling pathway protein 3 isoform 1; wnt-1 signaling pathway protein 3; Wnt1 signaling pathway protein 3; Wnt-1 inducible signaling pathway protein 3 Subclass: WNT1 inducible signaling pathway protein 3 isoform 2; wnt-1 signaling pathway protein 3; Wnt1 signaling pathway protein 3; Wnt-1 inducible signaling pathway protein 3 Subclass: bA69J8.1 (connective tissue growth factor)
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15	NM_011812 NP_035942.1	U:(C-D) +2.1	glycoprotein Subclass: Fibulin Subclass: EGF-containing fibulin-like extracellular matrix protein 2 precursor (Fibulin-4) (FBL-4) (UPH1 protein). Subclass: fibulin 5 precursor; urine p50 protein; developmental arteries and neural crest epidermal growth factor-like Subclass: EGF-containing fibulin-like extracellular matrix protein 1 isoform a precursor; fibrillin-like Subclass: EGF-containing fibulin-like extracellular matrix protein 1 isoform b; fibrillin-like Subclass: fibulin 1 Subclass: fibulin 2
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25	NM_011391 NP_035521.1	U:(C-D) +2.08	Monocarboxylate transporter Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 7; Monocarboxylate transporter 2 (MCT 2).

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			Subclass: monocarboxylate transporter isoform 1
			Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 1
			Subclass: monocarboxylate transporter 1
			Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 3; monocarboxylate transporter 3
			Subclass: Monocarboxylate transporter 3 (MCT 3).
			Subclass: solute carrier 16 (monocarboxylic acid transporters), member 8; monocarboxylate transporter 3
			Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 5; monocarboxylate transporter 5
	NM_010225 NP_034355.1	U:(C-D) +2.08	Transcription factor
			Subclass: forkhead box transcription factor
			Subclass: forkhead box F1; forkhead (Drosophila)-like 5; Forkhead, drosophila, homolog-like 5; forkhead-related activator 1
			Subclass: forkhead box F2; forkhead (Drosophila)-like 6
	NM_011851 NP_035981.1	U:(C-D) +2.08	nucleotidase
			Subclass: 5' nucleotidase, ecto; Purine 5-Prime-Nucleotidase; 5' nucleotidase (CD73); ecto-5'-nucleotidase
	NM_019759 NP_062733.1	U:(C-D) +2.07	Regulator of extracellular matrix formation
			Subclass: dermatopontin
	NM_011456 NP_035586.1	U:(C-D) +2.06	proteinase inhibitor
			Subclass: serine (or cysteine) proteinase inhibitor
			Subclass: serine (or cysteine) proteinase inhibitor, clade B
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1; protease inhibitor 2 (anti-elastase), monocyte/neutrophil; protease inhibitor 2 (anti-elastase), monocyte/neutrophil derived
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; plasminogen activator inhibitor, type II (arginine-serpin)
			Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3; squamous cell carcinoma antigen 1

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		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4; protease inhibitor (leucine-serpin); squamous cell carcinoma antigen 2; leupin
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5; protease inhibitor 5 (maspin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6; protease inhibitor 6 (placental thrombin inhibitor)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7; mesangium predominant gene, megin
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8; protease inhibitor 8 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9; protease inhibitor 9 (ovalbumin type)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10; protease inhibitor 10 (ovalbumin type, bomapin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 11
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12
		Subclass: serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13; hurpin; protease inhibitor 13 (hurpin, headpin)
10		Subclass: serine (or cysteine) proteinase inhibitor, clade A
		Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1; Protease inhibitor (alpha-1-antitrypsin); protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin
		Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
		Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)
15		Subclass: serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1; antithrombin III
	NM_008880	U:(C-D)
	NP_032906.1	+2.06
		Apoptosis-associated enzyme
		Subclass: phospholipid scramblase
		Subclass: phospholipid scramblase 1
		Subclass: phospholipid scramblase 2
		Subclass: Phospholipid scramblase 3 (PL scramblase 3) (Ca(2+)-dependent phospholipid scramblase 3).
		Subclass: phospholipid scramblase 4
	NM_008796	U:(C-D)
	NP_032822.1	+2.05
25		phosphatidylcholine transfer protein
		Subclass: Phosphatidylcholine transfer protein (PC-TP) (StAR-related lipid transfer protein 2) (StARD2) (START domain-containing protein 2).

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5	NM_011717 NP_035847.1	U:(C-D) +2.04	Protein containing widely-interspaced zinc finger motifs Subclass: WIZ protein Subclass: Human homolog of Mus musculus wizL protein [AA 4-1561] Subclass: Human homolog of Mus musculus wizS protein [AA 64-934]
10	NM_009197 NP_033223.1	U:(C-D) +2.04	monocarboxylic acid transporter Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 2; X-linked PEST-containing transporter Subclass: solute carrier family 16 (monocarboxylic acid transporters), member 10; T-type amino acid transporter 1
15	NM_009632 NP_033762.1	U:(C-D) +2.04	Polymerase Subclass: Poly [ADP-ribose] polymerase Subclass: Poly [ADP-ribose] polymerase-2 (PARP-2) (NAD(+) ADP-ribosyltransferase-2) (Poly[ADP-ribose] synthetase-2) (pADPRT-2) (hPARP-2). Subclass: Poly [ADP-ribose] polymerase-1 (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase-1) (Poly[ADP-ribose] synthetase-1). Subclass: poly(ADP-ribose)transferase; ADP-ribosyltransferase NAD(+); poly(ADP-ribose) synthetase Subclass: poly (ADP-ribose) transferase-like 3; ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 2; poly(ADP-ribose) synthetase
20	NM_011176 NP_035306.2	U:(C-D) +2.03	Serine protease Subclass: matriptase; suppression of tumorigenicity 14 (colon carcinoma); membrane-type serine protease; serine protease TADG-15; tumor associated differentially expressed gene 15 protein Subclass: prostamin Subclass: matriptase-2 Subclass: serine protease SINC19 Subclass: type II transmembrane serine protease 6; membrane-bound mosaic serine proteinase matriptase-2
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			Subclass: enterokinase
			Subclass: DESC1 protein
			Subclass: Atrial natriuretic peptide-converting enzyme (pro-ANP-converting enzyme) (Corin) (Heart specific serine proteinase ATC2).
			Subclass: epitheliasin
			Subclass: androgen-regulated serine protease TMPRSS2
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	NM_008797	U:(C-D)	
	NP_032823.1	+2.03	Carboxylase
			Subclass: Pyruvate carboxylase.
10			Subclass: Propionyl-Coenzyme A carboxylase, alpha polypeptide precursor
			Subclass: methylcrotonyl-Coenzyme A carboxylase 1 (alpha); 3-methylcrotonyl-CoA carboxylase biotin-containing subunit
			Subclass: acetyl-CoA carboxylase
	NM_013648	U:(C-D)	
	NP_038676.1	+2.02	Endoplasmic reticulum protein
15			Subclass: reticulon 1; neuroendocrine-specific protein
			Subclass: reticulon 2
			Subclass: RTN2-B
			Subclass: RTN2-C
			Subclass: neuroendocrine-specific protein B
20			Subclass: neuroendocrine-specific protein C - human
	NM_007743	U:(C-D)	Collagen
	NP_031769.1	+2	
			Subclass: type I collagen
25			Subclass: alpha 2 type I collagen; Collagen I, alpha-2 polypeptide; Collagen of skin, tendon and bone, alpha-2 chain
			Subclass: alpha 1 type I collagen preproprotein; Collagen I, alpha-1 polypeptide; osteogenesis imperfecta type IV; collagen of skin, tendon and bone, alpha-1 chain
			Subclass: alpha 1 type II collagen isoform 2, preproprotein; collagen II, alpha-1 polypeptide; cartilage collagen; chondrocalcin, included; COL11A3, formerly

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			Subclass: alpha 1 type III collagen; Collagen III, alpha-1 polypeptide; collagen, fetal
			Subclass: alpha 2 type V collagen
			Subclass: alpha 2 type V collagen preproprotein; Collagen V, alpha-2 polypeptide; AB collagen; collagen, fetal membrane, A polypeptide
			Subclass: Collagen alpha 1 type XI
			Subclass: Collagen alpha 1(XI) chain
			Subclass: Collagen alpha 1 type XI isoform A preproprotein; collagen XI, alpha-1 polypeptide
			Subclass: alpha 1 type XI collagen isoform B preproprotein; collagen XI, alpha-1 polypeptide
			Subclass: alpha 1 type XI collagen isoform C preproprotein; collagen XI, alpha-1 polypeptide
10	NM_023873	U:(C-D)	
	NP_076362.1	+1.9	p10-binding protein
	NM_011905	U:(C-D)	
	NP_036035.1	+1.6	Cell surface receptor
			Subclass: Toll-like receptor
			Subclass: toll-like receptor 2; toll/interleukin 1 receptor-like 4
			Subclass: toll-like receptor 1; Toll/interleukin-1 receptor-like
			Subclass: toll-like receptor 10
			Subclass: toll-like receptor 6
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	NM_010721	U:(C-D)	lamin
	NP_034851.1	7.08	
			Subclass: lamin B1.
			Subclass: Similar to lamin B1
			Subclass: Lamin B2
			Subclass: lamin A/C isoform 2; 70 kDa lamin
			Subclass: Similar to lamin A/C
			Alternate: lamin A protein
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NM_026228	U:(C-D)	protein up-regulated by BCG-CWS
NP_080504.1	4.88	
		Alternate: unnamed protein product
		Alternate: KIAA0062
		Alternate: similar to KIAA0062
		Alternate: Unknown (protein for MGC:23235)
NM_026156	U:(C-D)	similar to PP3898
NP_080432.1	3.75	
		Alternate: XAB2
		Alternate: KIAA1177 protein
		Alternate: HCNP protein; XPA-binding protein 2
		Alternate: Similar to HCNP protein; XPA-binding protein 2
		Alternate: FLJ00081 protein
U70139	U:(C-D)	nocturnin
AAB62717.1	3.08,	
	U:(HI-D)	
) 2.08	
		Alternate: CCR4 carbon catabolite repression 4-like (<i>S. cerevisiae</i>); CCR4-like (carbon catabolite repression 4, <i>S. cerevisiae</i>)
NM_008137	U:(C-D)	guanine nucleotide binding protein (G protein)
NP_032163.1	3.01	
		Subclass: guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide-binding protein 14
		Subclass: GTP-binding protein alpha q
		Subclass: Guanine nucleotide-binding protein G(Y), alpha subunit (Alpha-11)
		Subclass: guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
		Subclass: similar to GNA15; ALPHA-16
		Subclass: similar to Guanine nucleotide-binding protein, alpha-11 subunit (GL2)
		Subclass: Guanine nucleotide-binding protein G(O), alpha subunit 2

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		Subclass: guanine nucleotide binding protein alpha oB
		Subclass: Guanine nucleotide-binding protein G(i), alpha-1 subunit (Adenylate cyclase-inhibiting G alpha protein)
		Subclass: Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
		Subclass: guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3; 87U6
		Subclass: similar to Guanine nucleotide-binding protein G(T), alpha-3 subunit (Gustducin alpha-3 chain)
AK009292	U:(C-D)	
BAB26196.1	2.94, U:(HI-D)	
) 2.87	solute carrier family 27 (fatty acid transporter)
		Subclass: solute carrier family 27 (fatty acid transporter), member 4; fatty acid transport protein 4
		Subclass: solute carrier family 27 (fatty acid transporter), member 5; very long-chain acyl-CoA synthetase homolog 2; very long-chain acyl-CoA synthetase-related protein; likely ortholog of mouse solute carrier family 27 (fatty acid transporter), member 5
		Subclass: solute carrier family 27 member 3; fatty acid transport protein 3
		Subclass: solute carrier family 27 (fatty acid transporter), member 2; very long-chain fatty-acid-coenzyme A ligase 1; very-long-chain acyl-CoA synthetase
		Alternate: Unknown (protein for MGC:16752)
		Alternate: very long-chain acyl-CoA synthetase homolog 1
		Alternate: Unknown (protein for IMAGE:3613739)
		Alternate: Similar to hypothetical protein MGC4365
M12573	U:(C-D)	
AAA37863.1	2.94	heat shock 70kDa protein
		Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
		Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
		Subclass: heat shock 70kD protein 1-like
		Subclass: heat shock 70kDa protein 6 (HSP70B')
		Subclass: heat shock 70kDa protein 2; heat shock 70kD protein 2; Heat-shock 70kD protein-2

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AK017185	U:(C-D)	Ras-related protein Rab-30
BAB30625.1	2.9	
AK018132	U:(C-D)	KIAA1001 protein
BAB31086.1	2.44	
		Alternate: Similar to KIAA1001 protein
		Alternate: Arylsulfatase A; Chain: P; Synonym: Cerebroside-3-Sulfate-Sulfatase; Ec: 3.1.6.8
		Alternate: Similar to arylsulfatase A
		Alternate: N-acetylgalactosamine-6-sulfatase precursor; Galactosamine (N-acetyl)-6-sulfate sulfatase; chondroitinase
		Alternate: Unknown (protein for MGC:24090)
		Alternate: arylsulfatase F
		Alternate: similar to arylsulfatase F
		Alternate: Unknown (protein for MGC:31932)
		Alternate: arylsulfatase D precursor, isoform a
AK004984	U:(C-D)	cytochrome P450, subfamily IID, polypeptide 6; debrisoquine 4-hydroxylase; microsomal monooxygenase; xenobiotic
BAB23719.1	2.38	monooxygenase; flavoprotein-linked monooxygenase
AK013002	U:(C-D)	general transcription factor IIF, polypeptide 1 (74kD subunit)
BAB28588.1	2.21	
		Alternate: RAP74
		Alternate: Transcription Initiation Factor Iif, Subunit; Chain: A, C, E, G; Fragment: Residues 2-119; Synonym: Transcription
		Initiation Factor Rap30
AK007293	U:(C-D)	KIAA1879 protein
BAB24937.1	2.19, U:(HI-D)	
	2.62	
NM_019521	U:(C-D)	growth arrest-specific 6; AXL stimulatory factor
NP_062394.1	2.14	
		Alternate: protein S (alpha); Protein S, alpha

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		Alternate: Vitamin K-dependent protein S precursor	
NM_011693	U:(C-D)		
NP_035823.1	2.08	vascular cell adhesion molecule	
		Subclass: vascular cell adhesion molecule 1, isoform a ; CD106 antigen	
		Subclass: vascular cell adhesion molecule 1, isoform b precursor; CD106 antigen	
		Subclass: Vascular Cell Adhesion Protein 1; Chain: A; Fragment: Vcam-D1, D2 (Integrin Binding Fragment); Synonym: Vcam-1	
		Subclass: Vascular Cell Adhesion Molecule-1; Chain: A, B; Fragment: N-Terminal Two-Domain Fragment; Synonym: Vcam-1;	
		Engineered: Yes; Mutation: Y196D; Other_Details: Hybrid Molecule Composed Of Vcam-1 Domains 1 and 2 Fused To IgG, Hinge and Fc	
U70210	U:(C-D)	Amyloid beta A4 precursor protein-binding family B (Fe65-like protein)	
AAC53593.1	2.06		
		Subclass: Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	
		Subclass: similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	
		Subclass: amyloid beta A4 precursor protein-binding, family B, member 1 isoform delta E9; amyloid beta A4 precursor protein-binding, family B, member 1; stat-like protein; adaptor protein FE65a2	
		Subclass: adaptor protein FE65a2	
		Subclass: FE65-like protein 2 isoform a; amyloid precursor interacting protein	
		Subclass: Similar to FE65-LIKE 2	
		Subclass: FE65-like protein 2 isoform b; amyloid precursor interacting protein	
		Subclass: FE65-like protein 2 isoform c; amyloid precursor interacting protein	
		transient receptor potential cation channel	
NM_020277	U:(C-D)		
NP_064673.1	2.05,		
	U:(HI-D)		
) 2.32		
		Subclass: transient receptor potential cation channel, subfamily M, member 5; MLSN1 and TRP-related; MLSN1- and TRP-related; LTRPC5 protein	
		Subclass: transient receptor potential cation channel, subfamily M, member 4	
		Subclass: transient receptor potential-related channel 7, a novel putative Ca2+ channel protein	

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			Subclass: transient receptor potential cation channel, subfamily M, member 2; transient receptor potential-related channel 7, a novel putative Ca2+ channel protein; transient receptor potential channel 7
			Subclass: transient receptor potential cation channel, subfamily M, member 8
			Subclass: transient receptor potential cation channel, subfamily M, member 6
			Subclass: transient receptor potential cation channel, subfamily M, member 1; melastatin 1 [
5			Subclass: TRP-related cation influx channel
			Subclass: channel-kinase 1
			Subclass: similar to LTRPC7
			Alternate: melastatin 1
10	NM_011676	U:(C-D)	unc119 (C.elegans) homolog, isoform a; unc119 (C.elegans) homolog; retinal protein 4
	NP_035806.1	2.04	
			Alternate: unc119 (C.elegans) homolog, isoform b; unc119 (C.elegans) homolog; retinal protein 4
	AF241249	U:(C-D)	Unknown (protein for MGC:16590)
	AAG02285.1	2.03	
15			Alternate: Unknown (protein for IMAGE:3029289)
			Alternate: FLJ00103 protein
			Alternate: similar to FLJ00103 protein
			Alternate: Unknown (protein for MGC:20519)
			Alternate: KIAA1863 protein
20			Alternate: unnamed protein product
	NM_010220	U:(C-D)	FK506-binding protein
	NP_034350.1	2.02	
			Subclass: FK506-binding protein 5; 51 kDa FK506-binding protein 5; 54 kDa progesterone receptor-associated immunophilin; T-cell FK506-binding protein; peptidylprolyl cis-trans isomerase; rotamase; FF1 antigen; HSP90-binding immunophilin
			Subclass: FK506-binding protein 4; FK506-binding protein 4 (59kD); T-cell FK506-binding protein, 59kD; p59 protein; HSP binding immunophilin; peptidylprolyl cis-trans isomerase; rotamase; FK506 binding protein 4 (59kD)
25			Subclass: similar to FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (p59 protein) (HSP binding immunophilin) (HBI) (FKBP52 protein) (52 kDa FK506 binding protein) (FKBP59)

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NM_016696	U:(C-D)	
NP_057905.1	2.02	glypican
		Subclass: glypican 1
		Subclass: glypican 6
		Subclass: glypican 4
		Subclass: similar to Glypican-2 (Cerebroglycan) (HSPG M13)
NM_013692	U:(C-D)	
NP_038720.1	2.01	TGFB inducible early growth response
		Alternate: EGR alpha transcription factor - human
		Alternate: TGFB inducible early growth response 2
AK004865	U:(C-D)	
BAB23626.1	2	HMG CoA synthase (3-hydroxy-3-methylglutaryl-Coenzyme A synthase)
		Subclass: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
		Subclass: 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble); 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
		Subclass: hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5), cytosolic, fibroblast isoform
		Subclass: similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase)
NM_019810	U:(C-D)	
NP_062784.1	2	Sodium/glucose cotransporter.
		Subclass: solute carrier family 5 (sodium/glucose cotransporter), member 1; Human Na ⁺ /glucose cotransporter 1 mRNA, complete cds; solute carrier family 5 (sodium/glucose cotransporter), member 1
		Subclass: solute carrier family 5 (low affinity glucose cotransporter), member 4; solute carrier family 5 (neutral amino acid transporters, system A), member 4; low affinity sodium glucose cotransporter
		Subclass: solute carrier family 5 (sodium/glucose cotransporter), member 2; solute carrier family 5 (sodium/glucose cotransporter), member 2
		Subclass: solute carrier family 5 (inositol transporters), member 3; solute carrier family 5 (inositol transporter), member 3; human solute carrier family 5, member 3, Sodium/myo-inositol cotransporter; sodium/myo-inositol cotransporter 1

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			Subclass: dJ1024N4.1 (novel Sodium:solute symporter family member similar to SLC5A1 (SGLT1))
			Subclass: sodium/myo-inositol cotransporter 2; putative sodium-coupled cotransporter RKST1; homolog of rabbit KST1
			Subclass: putative sodium-coupled cotransporter RKST1
			Subclass: similar to 597 aa protein related to Na/glucose cotransporters
			Subclass: Sodium/myo-inositol cotransporter (Na(+)/myo-inositol cotransporter)
			Alternate: hypothetical protein FLJ25217
NM_028780	U:(C-D)		transmembrane 9 superfamily
NP_083056.1	2		Subclass: transmembrane 9 superfamily member 1; multispinning membrane protein (70kD); transmembrane protein 9 superfamily member 1
			Subclass: transmembrane 9 superfamily member 2; 76 kDa membrane protein; transmembrane protein 9 superfamily member 2
			Subclass: similar to Transmembrane 9 superfamily protein member 3 precursor (SM-11044 binding protein) (EP70-P-iso)
			Subclass: transmembrane protein TM9SF3
			Alternate: SM-11044 binding protein
			Alternate: KIAA0255 gene product
			Alternate: endomembrane protein emp70 precursor isolog
			Alternate: unnamed protein product
			Alternate: unnamed protein product
NM_009252	U:(C-D)		proteinase inhibitor
NP_033278.1	1.77		Subclass: alpha1-antichymotrypsin
			Subclass: similar to Alpha-1-antichymotrypsin precursor (ACT)
			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
			Subclass: chymotrypsin inhibitor
			Subclass: Cleaved Antichymotrypsin A347R
			Subclass: Cleaved Antichymotrypsin A349R
			Subclass: Cleaved Antichymotrypsin T345R

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			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 4; protease inhibitor 4 (kallistatin)
			Subclass: Kallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4)
			Subclass: serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 5; Protein C inhibitor (plasminogen activator inhibitor-3); protein C inhibitor; protein C inhibitor (plasminogen activator inhibitor III)
			Subclass: protein C inhibitor
			Subclass: plasma serine protease inhibitor precursor
			Subclass: Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 1
			Subclass: acrosomal serine protease inhibitor
			Alternate: hypothetical protein DKFZp434P131.1
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	AK017185	U;(C-D)	
	BAB30625.1	+2.9	Ras-related protein
			Subclass: Ras-related protein Rab-30
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	NM_011704	U	
	NP_035834.1	(C-HI)	
		4.37, U	
		(C-D)	
		3.14, U	
		(HI-D)	
		2.37	Vanin
			Vanin 1 (VNN1); pantetheinase
15			vanin 3 isoform 1 ; VNN3 protein; pantetheinase
			vanin 2, isoform 1 ; Vannin 2; pantetheinase
			vanin 2, isoform 2; Vannin 2; pantetheinase
			Alternate: Biotinidase
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NM_007468 NP_031494.1	U (C-HI) 2.98, U (C-D) 2.42, U (HI-D) 2.16	Apolipoprotein A-IV (Apo-AIV)
NM_016974 NP_058670.1	U (C-HI) 2.79, U (C-D) 4.24, U (HI-D) 2.47	D-site-binding protein (Albumin D box-binding protein) (TAXREB302)
NM_019634 NP_062608.1	U:(HI- D) 2.86	transmembrane 4 superfamily Subclass: transmembrane 4 superfamily member 2; membrane component, x chromosome, surface marker 1; T-cell acute lymphoblastic leukemia associated antigen 1; transmembrane protein A15; tetraspanin protein; cell surface glycoprotein A15; CD231 antigen; transmembrane 4 superfamily 2b Subclass: transmembrane 4 superfamily member 6; tetraspanin TM4SF; A15 homolog; tetraspanin TM4-D; tetraspanin 6
NM_008597 NP_032623.1	U:(HI- D) 2.36	matrix Gla protein
NM_009234 NP_033260.1	U:(HI- D) 2.36	SRY (sex determining region Y)-box 11; SRY (sex-determining region Y)-box 11

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NM_009964 NP_034094.1	U:(HI- D) 2.06	crystallin, alpha B; crystallin, alpha-2; Rosenthal fiber component; heat-shock 20 kD like-protein
NM_013565 NP_038593.1	U:(HI- D) 2.05	integrin alpha
		Subclass: VLA-3 alpha subunit
		Subclass: integrin alpha-3 (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c)
		Subclass: integrin alpha 3 isoform b
		Subclass: integrin alpha 6
		Subclass: integrin alpha-6 chain precursor, splice form A
		Subclass: integrin alpha-6 chain precursor, splice form B
		Subclass: integrin alpha 7
NM_013805 NP_038833.1	U:(HI- D) 2.04	transmembrane protein claudin 5; androgen withdrawal and apoptosis induced protein RVP1 (rat)-like; Claudin-5 (transmembrane protein deleted in velocardiocfacial syndrome)
AK014697 BAB29508.1	U:(HI- D) 2.01	DC-specific transmembrane protein
AK007868 BAB25319.1	U:(C-HI) +3.19 U:(C-D) +2.42	chromosome 11 open reading frame 24
NM_017480 NP_059508.1	U:(C-HI) 6.6	inducible T-cell co-stimulator; activation-inducible lymphocyte immunomodulatory molecule; inducible costimulator
M12571 AAA57234.1	U:(C-HI) 3.58	Alternate: Similar to inducible T-cell co-stimulator heat shock 70kDa protein

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		Subclass: heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-induced protein; dnaK-type molecular chaperone HSP70-1
		Subclass: heat shock 70kDa protein 1B; heat shock 70kD protein 1B
		Subclass: heat shock 70kD protein 1-like
		Subclass: heat shock 70kDa protein 6 (HSP70B')
		Subclass: heat shock 70kDa protein 2; Heat-shock 70kD protein-2
NM_007585	U:(C-HI	Annexin
NP_031611.1) 3.49,	
	U:(C-D)	
	4.83	
		Subclass: annexin A2; annexin II; lipocortin II; Annexin II (lipocortin I); calpactin I, heavy polypeptide (p36); annexin II (lipocortin II); calpactin I, heavy polypeptide); annexin II (lipocortin II)
		Subclass: bA255A11.8 (novel protein similar to annexin A2 (ANXA2) (lipocortin II, calpactin I heavy chain, chromobindin 8, PAP-IV))
		Subclass: annexin I; annexin I (lipocortin I); lipocortin I
		Subclass: Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedlin) (Carbohydrate-binding protein P33/P41) (P33/41)
		Subclass: annexin A11; annexin XI; autoantigen, 56-kD; calcyclin-associated annexin 50
		Subclass: annexin VI isoform 2; annexin VI (p68); calcium-binding protein p68; calphobindin II;
		Subclass: annexin VI isoform 1; annexin VI (p68); calcium-binding protein p68; calphobindin II; calelectrin F498
		Subclass: Annexin III
		Subclass: annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III, 1,2-cyclic-inositol-phosphate phosphodiesterase, placental anticoagulant protein III, calcimedlin 35-alpha); calcimedlin 35-alpha
		Subclass: Annexin V (Lipocortin V, Endonexin II, Placental Anticoagulant Protein) (Calcium Ions Are Visible) Mutation With Glu 17 Replaced By Gly (E17G)
		Subclass: annexin A5
		Subclass: annexin VIII; Annexin VII
		Subclass: similar to annexin A8
		Subclass: annexin VII isoform 2; annexin VII (synexin); synexin

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		Subclass: annexin VII isoform 1; annexin VII (synexin); synexin
		Subclass: annexin A13 isoform b
		Subclass: annexin A13; annexin XIII; annexin, intestine-specific
		Subclass: annexin 31; annexin XXXI
		Subclass: keratinocyte annexin-like protein
		Alternate: protein PP4-X
		Alternate: protein p68 (1 - 673)
NM_007980 NP_032006.1	U:(C-HI) 3.49, U:(C-D) 2.22	intestinal fatty acid binding protein 2; Fatty acid-binding protein, intestinal; I-FABP; fatty acid binding protein 2, intestinal
NM_007809 NP_031835.1	U:(C-HI) 3.41, U:(C-D) 3.69	cytochrome P450
		Subclass: cytochrome P450, subfamily XVII polypeptide; steroid 17-alpha-monooxygenase; steroid 17-alpha-hydroxylase/17,20 lyase; cytochrome p450 XVIIA1
		Subclass: cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1; flavoprotein-linked monooxygenase; cytochrome P1-450, dioxin-inducible; aryl hydrocarbon hydroxylase; P450 form 6; xenobiotic monooxygenase; microsomal monooxygenase
		Subclass: cytochrome P450-1A2
		Subclass: cytochrome P450 4
		Subclass: Cytochrome P450 XXIB (Steroid 21-hydroxylase) (P450-C21B)
		Subclass: cytochrome P450, subfamily XXIA polypeptide 2; steroid 21-monooxygenase; steroid 21-hydroxylase
		Subclass: cytochrome P450 CYP1B1

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AK007868	U:(C-HI	chromosome 11 open reading frame 24
BAB25319.1) 3.19,	
	U:(C-D)	
	2.42	
U67189	U:(C-HI	Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R) (A28-RGS14P)
AAB50619.1) 3.17	
M63245	U:(C-HI	aminolevulinate synthase
AAA91867.1) 3.05	
		Subclass: aminolevulinate synthase 1
		Subclass: 5-aminolevulinic acid synthase
		Subclass: 5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinic synthase) (Delta-ALA synthetase) (ALAS-E)
		Subclass: aminolevulinate, delta-, synthase 2; Aminolevulinate, delta-, synthase-2
		Subclass: Similar to aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)
NM_007437	U:(C-HI	
NP_031463.1) 3.02	Aldehyde dehydrogenase
		Subclass: similar to fatty aldehyde dehydrogenase
		Subclass: aldehyde dehydrogenase 3A2; aldehyde dehydrogenase 10; aldehyde dehydrogenase 3 family, member A2; fatty aldehyde dehydrogenase
		Subclass: aldehyde dehydrogenase 3 family, member A1; aldehyde dehydrogenase, dimeric NADP-preferring; acetaldehyde dehydrogenase; ALDH, stomach type
		Subclass: aldehyde dehydrogenase 3B1; aldehyde dehydrogenase 7; aldehyde dehydrogenase 3 family, member B1
		Subclass: Similar to aldehyde dehydrogenase 3 family, member B1
		Subclass: aldehyde dehydrogenase 3B2; aldehyde dehydrogenase 8; aldehyde dehydrogenase 3 family, member B2
		Subclass: Similar to aldehyde dehydrogenase 3 family, member B2

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NM_022331 NP_071726.1	U:(C-HI)) 3.00, U:(C-D) 2.29	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1; MMS-inducible gene
		Alternate: Similar to homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
NM_007837 NP_031863.1	U:(C-HI)) 2.98, U:(C-D) 2.16	DNA-damage-inducible transcript 3; C/EBP homologous protein; growth arrest- and DNA damage-inducible
		Alternate: TLS-CHOP
		Alternate: DNA-damage-inducible protein GADD153 - human
NM_007860 NP_031886.1	U:(C-HI)) 2.84, U:(C-D) 2.06	Type I iodothyronine deiodinase (Type-I 5'deiodinase) (DIO1) (Type 1 DI) (5DI)
		Alternate: Similar to deiodinase, iodothyronine, type I
AK007378 BAB24997.1	U:(C-HI)) 2.77	hypothetical protein MGC4504
NM_011375 NP_035505.1	U:(C-HI)) 2.65, U:(C-D) 2.16	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase); ganglioside G(M3) Synthase
		Alternate: Gal beta 1,3(4) GlcNAc alpha 2,3-sialyltransferase

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NM_007760	U:(C-HI	carnitine acetyltransferase
NP_031786.1) 2.57,	
	U:(C-D)	
	2.16	
		Subclass: Carnitine O-acetyltransferase (Carnitine acetylase) (CAT)
		Subclass: carnitine acetyltransferase isoform 1
		Subclass: carnitine acetyltransferase isoform 2
		Subclass: carnitine acetyltransferase isoform 3
NM_020570	U:(C-HI	X-ray repair cross complementing protein 2; X-ray repair, complementing defective, repair in Chinese hamster; DNA repair protein
NP_065595.1) 2.55	XRCC2
NM_019423	U:(C-HI	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
NP_062296.1) 2.53,	
	U:(C-D)	
	2.08	
		Alternate: elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4; Stargardt disease 3 (autosomal dominant)
NM_031162	U:(C-HI	CD3Z antigen, zeta polypeptide (TIT3 complex)
NP_112439.1) 2.49	
NM_019699	U:(C-HI	fatty acid desaturase
NP_062673.1) 2.46	
		Subclass: fatty acid desaturase 2; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2
		Subclass: fatty acid desaturase 3; delta-6 fatty acid desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 3
		Subclass: fatty acid desaturase 1; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5 desaturase; delta-5 fatty acid desaturase

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NM_023719 NP_076208.1	U:(C-HI)) 2.36; U:(C-D) 2.42	thioredoxin interacting protein; upregulated by 1,25-dihydroxyvitamin D-3
NM_013760 NP_038788.1	U:(C-HI)) 2.34, U:(C-D) 2.1	DnaJ (Hsp40) homolog, subfamily B, member 9; microvascular endothelial differentiation gene 1; DKFZP564F1862 protein; endoplasmic reticulum DnaJ homolog 4
		Alternate: similar to putative microvascular endothelial differentiation gene 1; similar to X98993 (PID:g1771560)
NM_023184 NP_075673.1	U:(C-HI)) 2.34	Kruppel-like factor 15; KKLf protein; kidney-enriched Kruppel-like factor
NM_018791 NP_061261.1	U:(C-HI)) 2.32	Zinc finger protein
		Subclass: zinc finger protein 93 homolog; zinc finger protein homologous to mouse Zfp93; zinc finger protein homologous to Zfp93 in mouse; zinc finger protein 93 homolog (mouse)
		Subclass: zinc finger protein 226; Kruppel-associated box protein
		Subclass: Zinc finger protein ZNF45
		Subclass: similar to Zinc finger protein 229
		Subclass: zinc finger protein 224
		Subclass: zinc finger protein 228
		Subclass: similar to ZNF228 protein
		Subclass: Zinc finger protein 234 (Zinc finger protein HZF4)
		Subclass: similar to Zinc finger protein 234 (Zinc finger protein HZF4)
		Subclass: zinc finger protein 225
AK007864 BAB25316.1	U:(C-HI)) 2.31	similar to RIKEN cDNA 1810054O13

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NM_019545	U:(C-HI)	hydroxyacid oxidase
NP_062418.1) 2.31	Subclass: hydroxyacid oxidase 3; medium-chain 2-hydroxy acid oxidase HAOX3; (S)-2-hydroxy-acid oxidase; glycolate oxidase
		Subclass: hydroxyacid oxidase 2; long-chain L-2-hydroxy acid oxidase; (S)-2-hydroxy-acid oxidase; glycolate oxidase
		Subclass: hydroxyacid oxidase 1; (S)-2-hydroxy-acid oxidase; glycolate oxidase
NM_011058	U:(C-HI)	platelet-derived growth factor receptor
NP_035188.1) 2.3	Subclass: platelet-derived growth factor receptor alpha polypeptide
		Subclass: platelet-derived growth factor receptor beta; beta platelet-derived growth factor receptor
		Alternate: vascular endothelial growth factor receptor
		Subclass: Vascular endothelial growth factor receptor 3 (VEGFR-3) (Tyrosine-protein kinase receptor FLT4)
		Subclass: vascular endothelial growth factor receptor 2
		Alternate: KIT protein
		Alternate: colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
		Alternate: Macrophage colony stimulating factor 1 receptor (CSF-1-R) (Fms proto-oncogene) (c-fms) (CD115 antigen)
		Alternate: FLT3 receptor tyrosine kinase
		Alternate: fms-related tyrosine kinase 3
		Alternate: fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
		Alternate: fms-related tyrosine kinase 4; fms-related tyrosine kinase-4 (vascular endothelial growth factor receptor 3)
NM_010565	U:(C-HI)	inhibin beta C chain preproprotein; activin beta-C chain
NP_034695.1) 2.28	Alternate: activin beta E
NM_011994	U:(C-HI)	ATP-binding cassette, sub-family D
NP_036124.1) 2.27	Subclass: ATP-binding cassette, sub-family D, member 2; adrenoleukodystrophy-like 1; hALDR
		Subclass: ATP-binding cassette, sub-family D (ALD), member 1; adrenoleukodystrophy protein
		Subclass: ATP-binding cassette, sub-family D, member 3; Peroxisomal membrane protein-1 (70kD); peroxisomal membrane protein 1 (70kD, Zellweger syndrome); peroxisomal membrane protein-1

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NM_018817 NP_061287.1	U:(C-HI)) 2.27	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a-like 1; HepA-related protein; SMARCA-like protein 1
AK006096 BAB24407.1	U:(C-HI)) 2.24	Similar to RIKEN cDNA 1700018O18 gene
NM_019682 NP_062656.1	U:(C-HI)) 2.24	dynein, cytoplasmic, light polypeptide; Dynein, cytoplasmic, light chain (protein inhibitor of neuronal NOS); protein inhibitor of neuronal nitric oxide synthase
NM_009154 NP_033180.1	U:(C-HI)) 2.23	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain (TM) and short cytoplasmic domain, 5A
		Alternate: KIAA1445 protein
		Alternate: similar to KIAA1445 protein
AK005274 BAB23924.1	U:(C-HI)) 2.22, U:(C-D) 2.15	hypothetical protein MGC2605
		Alternate: similar to hydroxyacyl glutathione hydrolase 2
NM_009315 NP_033341.1	U:(C-HI)) 2.2	TBP-associated factor 6 Subclass:
		Subclass: TBP-associated factor 6 isoform gamma; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit
		Subclass: TBP-associated factor 6 isoform delta; TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80 kD; TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD; transcription initiation factor TFIID 70 kD subunit

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NM_011361 NP_035491.1	U:(C-HI)) 2.2	serine/threonine protein kinase sgk (serum/glucocorticoid regulated kinase)
		Alternate: serum/glucocorticoid regulated kinase-like; cytokine-independent survival kinase
		Alternate: v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma); protein kinase B
NM_011844 NP_035974.1	U:(C-HI)) 2.19	monoglyceride lipase
NM_018861 NP_061349.1	U:(C-HI)) 2.18	solute carrier family 1 (glutamate/neutral amino acid transporter)
		Subclass: solute carrier family 1 (glutamate/neutral amino acid transporter), member 4; Solute carrier family 1 (glutamate/neutral amino acid transporter),
		Subclass: solute carrier family 1 (neutral amino acid transporter), member 5; baboon M7 virus receptor; RD114 virus receptor; neutral amino acid transporter B
		Alternate: sodium-dependent neutral amino acid transporter type 2 truncated isoform
		Alternate: neutral amino acid transporter B
AF213258 AAG43836	U:(C-HI)) 2.17, U:(C-D) 2.34	membrane-associated guanylate kinase-related 3
		Alternate: similar to membrane-associated guanylate kinase MAGI3
		Alternate: MAGI-1A
		Alternate: MAGI-1C beta
		Alternate: MAGI-1B alpha beta
		Alternate: dJ730K3.2 (similar to BAI1-associated protein)
		Alternate: atrophin-1 interacting protein 1; activin receptor interacting p; KIAA0705 gene product
		Alternate: BAI1-associated protein 1; WW domain-containing protein 3
		Alternate: brain-specific angiogenesis inhibitor-associated protein 1

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NM_008382	U:(C-HI	activin beta E
NP_032408.1) 2.13	
		Alternate: inhibin beta C chain preproprotein; activin beta-C chain
NM_007679	U:(C-HI	CCAAT/enhancer binding protein (C/EBP), delta
NP_031705.1) 2.11	
		Alternate: similar to CCAAT/enhancer binding protein delta (C/EBP delta) (Nuclear factor NF-IL6-beta) (NF-IL6-beta)
NM_030887	U:(C-HI	Jun dimerization protein
NP_112149.1) 2.07	
NM_009366	U:(C-HI	transforming growth factor beta-stimulated protein TSC-22
NP_033392.1) 2.06,	
	U:(C-D)	
	2.89,	
	U:(HI-D	
) 2.64	
		Alternate: cerebral protein-2
NM_019992	U:(C-HI	BCR downstream signaling 1
NP_064376.1) 2.06,	
	U:(C-D)	
	2.23,	
	U:(HI-D	
) 2.12	
NM_019415	U:(C-HI	Solute carrier family 12
NP_062288.1) 2.06	
		Subclass: Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter) (Na-Cl symporter)
		Subclass: solute carrier family 12 (sodium/potassium/chloride transporters), member 2; Solute carrier family 12
		(sodium/potassium/chloride transporters),
		Subclass: solute carrier family 12 (potassium/chloride transporters), member 7; potassium/chloride transporter KCC4

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			Subclass: solute carrier family 12, (potassium-chloride transporter) member 5
AK002693	U:(C-HI		diacylglycerol O-acyltransferase 2 like 1; diacylglycerol acyltransferase 2-like
BAB22288.1) 2.04		
AK003722	U:(C-HI		ubiquitin-conjugating enzyme E2C; ubiquitin carrier protein E2-C
BAB22959.1) 2.04		
NM_010516	U:(C-HI		CYR61 protein (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (GIG1 protein)
NP_034646.1) 2.04		
			Alternate: connective tissue growth factor
			Alternate: WNT1 inducible signaling pathway protein 1, isoform 1 precursor; Wnt1 signaling pathway protein 1; Wnt-1 inducible signaling pathway protein 1; wnt-1 signaling pathway protein 1; connective tissue growth factor related protein WISP-1; Wnt-1 induced secreted protein 1
			Alternate: WNT1 inducible signaling pathway protein 3, isoform 2; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3
			Alternate: WNT1 inducible signaling pathway protein 3, isoform 1; Wnt1 signaling pathway protein 3; lost in inflammatory breast cancer tumor suppressor protein; connective tissue growth factor like protein; connective tissue growth factor related protein WISP-3
NM_010354	U:(C-HI		gelsolin (amyloidosis, Finnish type); Gelsolin
NP_034484.1) 2.03		
			Alternate: scinderin; adseverin; KIAA1905 protein
			Alternate: villin 1; Villin-1
			Alternate: similar to mouse adseverin(D5); similar to PID:g2218019
			Alternate: Advillin (p92)
			Alternate: Similar to gelsolin (amyloidosis, Finnish type)
			Alternate: Similar to advillin

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AK002717 XP_134867	U:(C-HI) 2.02	RNA, U transporter 1; snurportin-1; snuportin-1
AK004600 BAB23401.1	U:(C-HI) 2.02	Rho guanine nucleotide exchange factor 3; RhoGEF protein; 59.8 kDa protein
		Alternate: Similar to Rho guanine nucleotide exchange factor (GEF) 3
M62766 AAA37819.1	U:(C-HI) 2.02	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
		Subclass: Similar to 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
NM_008299 NP_032325.1	U:(C-HI) 2.02	DnaJ (Hsp40) homolog
		Subclass: DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
		Subclass: similar to DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b; Heat shock protein J2
		Subclass: similar to DnaJ homolog subfamily B member 8 (mDJ6)
NM_010877 NP_035007.1	U:(C-HI) 2.02	Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH oxidase factor 2) (67 kDa neutrophil oxidase factor) (p67-phox)
		Alternate: Similar to neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2)
		Alternate: p67phox-like protein
NM_019643 NP_062617.1	U:(C-HI) 2.02	TERA protein
NM_013594 NP_038622.1	U:(C-HI) 2.01, U:(C-D) 2.15	methyl-CpG binding protein 1
		Subclass: methyl-CpG binding domain protein 1 isoform 1
		Subclass: methyl-CpG binding protein splice variant 1

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		Subclass: methyl-CpG binding domain protein 1 isoform 2
		Subclass: methyl-CpG binding protein splice variant 2
		Subclass: methyl-CpG binding domain protein 1 isoform PCM1
		Subclass: methyl-CpG binding domain protein 1 isoform 3
		Subclass: methyl-CpG binding domain protein 1 isoform 4
NM_025566	U:(C-HI	hypothetical protein MGC17791
NP_079842.1) 2	
		Alternate: similar to RIKEN cDNA 2600017J23
AK004002	U:(C-HI	five-lipoxygenase activating protein (FLAP)
BAB23117.1) 2	
NM_021366	U:(C-HI	Kruppel-like factor 13; transcription factor NSLP1; novel Sp1 like zinc finger transcription factor; RANTES factor of late activated T
NP_067341.1) 2	lymphocytes-1; basic transcription element binding protein 3
		Alternate: similar to Krueppel-like factor 13 (Transcription factor BTEB3) (Basic transcription element binding protein 3)
		(BTE-binding protein 3) (RANTES factor of late activated T lymphocytes-1) (RFLAT-1) (Transcription factor NSLP1) (Novel
		Sp1-like zinc fi
NM_025566	U:(C-HI	hypothetical protein MGC17791
NP_079842.1) +2	
		Alternate: similar to RIKEN cDNA 2600017J23

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Master Table 2: Subtable 2C Classes of Mixed Genes/Proteins

Mouse Gene Protein	Behavior	Human Protein Name
NM_016875	U:(HI-D)	germ cell specific Y-box binding protein; contrin
NP_058571.1	2.73	
	F:(C-D)	
	-4.72	
AF001293	U:(HI-D)	zinc finger protein, Subclass: similar to zinc finger protein, subfamily 1A, 3 (Aiolos) Subclass: zinc finger protein, subfamily 1A, 3 (Aiolos) Subclass: AIOLOS isoform four Subclass: AIOLOS isoform two Subclass: AIOLOS isoform three Subclass: AIOLOS isoform six Subclass: AIOLOS isoform five Subclass: zinc finger protein, subfamily 1A, 1 (Ikaros); Ikaros (zinc finger protein) Subclass: zinc finger protein, subfamily 1A, 2 (Helios); zinc finger DNA binding protein Helios Subclass: Similar to zinc finger protein, subfamily 1A, 2 (Helios) Subclass: zinc finger protein, subfamily 1A, 4 (Eos); zinc finger transcription factor Eos
AAB58795.1	2.59	
	F:(C-D)	
	-3.71	
NM_009895	U:(HI-D)	cytokine-inducible SH2-containing protein
NP_034025.1	2.45	
	F:(C-D)	
	-2.25	

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			Subclass: cytokine-inducible SH2-containing protein isoform 2; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling
			Subclass: cytokine-inducible SH2-containing protein isoform 1; cytokine-inducible SH2-containing protein; cytokine-inducible inhibitor of signaling type 1B; suppressor of cytokine signaling
NM_018830	U:(H-I-D)		N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2; N-acylsphingosine amidohydrolase 2; mitochondrial ceramidase; N-acylsphingosine amidohydrolase (acid ceramidase) 2
NP_061300.1	2.42		
	F:(C-D)		
	-2.62		
AF398969	U:(H-I-D)		ankyrin repeat and SOCS box-containing 8
AAK97491.1	2.35		
	F:(C-D)		
	-2.5		
NM_016970	U:(H-I-D)		killer cell lectin-like receptor subfamily G, member 1; mast cell function-associated antigen (ITIM-containing)
NP_058666.1	2.13		
	F:(C-D)		
	-2.74		
NM_009344	U:(H-I-D)		pleckstrin homology-like domain, family A, member 1; PQ-rich protein
NP_033370.1	2.1		
	F:(C-D)		
	-3.91		
			Alternate: Similar to T-cell death associated gene
NM_009255	U:(H-I-D)		similar to tropomyosin, fibroblast - human
NP_033281.1	2.01		
	F:(C-D)		
	-2.61		
			Alternate: Protease Inhibitor; Proteinase Inhibitor
			Subclass: Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1) (Protease inhibitor 7)
			Subclass: Plasminogen Activator Inhibitor-1; Chain: A; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai

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		Subclass: serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1; plasminogen activator inhibitor, type I; Synonym: Pai-1, Endothelial Plasminogen Activator Inhibitor, Pai
		Subclass: prebeta-migrating plasminogen activator inhibitor
		Subclass: Cleaved Substrate Variant Of Plasminogen Activator Inhibitor-1
		Subclass: Active Form Of Human Pai-1
		Subclass: serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1; protease inhibitor 12 (neuroserpin)
		Subclass: serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1
		Subclass: protease inhibitor 14; pancpin
NM_020013	U:(C-HI)	fibroblast growth factor 21
NP_064397.1	6.00, U:(C-D) 5.03, F:(HI-D) -3.06	
X82786	U:(C-HI)	antigen identified by monoclonal antibody Ki-67; Proliferation-related Ki-67 antigen
CAA58026.1	4.07, F:(HI-D) -4.25	
NM_010000	U:(C-HI)	cytochrome P450
NP_034130.1	34.21, U:(C-D) 8.32, F:(HI-D) -3.81	
		Subclass: cytochrome P450-2B6
		Subclass: Cytochrome P450 2A13 (CYP1A13)

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			Subclass: cytochrome P450 2A6
			Subclass: P-450 IIA3 protein (1 is 3rd base in codon)
			Subclass: cytochrome P450 2A4
			Subclass: Cytochrome P450 2A7 (CYP1IA7) (P450-IIA4)
			Subclass: cytochrome P450 2C8
			Subclass: cytochrome P450 2F1
			Subclass: cytochrome P450 2C18
			Subclass: cytochrome P450 2C9
			Subclass: cytochrome P450 2C10
			Subclass: cytochrome P450 2C19
			Subclass: cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7 isoform 1
NM_009689	U:(C-HI)		baculoviral IAP repeat-containing protein 5; apoptosis inhibitor 4; survivin
NP_033819.1	3.67;		
	F:(HI-D)		
	-3.5		
			Alternate: survivin-beta
NM_010634	U:(C-HI)		fatty acid binding protein 5 (psoriasis-associated); E-FABP
NP_034764.1	3.17;		
	F:(HI-D)		
	-5.62		
NM_007659	U:(C-HI)		
NP_031685.1	3.00;		
	F:(HI-D)		
	-2.87		Protein Kinase
			Subclass: cell division cycle 2 protein, isoform 1; cell division control protein 2 homolog; cyclin-dependent kinase 1; p34 protein kinase; cell cycle controller CDC2

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		Subclass: cyclin-dependent kinase 3
		Subclass: Pcdk2/Cyclin A In Complex With Mgadp, Nitrate and Peptide Substrate
		Subclass: Cyclin-Dependent Kinase-2; Chain: A, C; Synonym: Cdk2; Ec: 2.7.1.-
		Subclass: Cell Division Protein Kinase 2; Chain: A; Synonym: Cyclin Dependent Kinase 2; Ec: 2.7.1.37
		Subclass: PCTAIRE protein kinase 2; serine/threonine-protein kinase PCTAIRE-2; protein kinase cdc2-related PCTAIRE-2
		Subclass: Cdk5-P25(Nck5A) Complex - Protein Kinase II Catalytic Subunit, Cdk5 - Cdk5 Activator 1, Cyclin-Dependent Kinase 5 Regulatory Subunit 1, Protein Kinase II 23 Kda Subunit, Tpkii Regulatory Subunit, P23, P25, P35
NM_007822	U:(C-HI)	cytochrome P450,
NP_031848.1	24.5, F:(C-D) -5.06, F:(HI-D) -7.06	
		Subclass: cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase (CYP4A11)
		Subclass: cytochrome P450, subfamily IVB, polypeptide 1; cytochrome P450, subfamily IVB, member 1; microsomal monooxygenase
		Subclass: cytochrome P450, subfamily IVF, polypeptide 2; leukotriene B4 omega-hydroxylase; leukotriene-B4 20-monooxygenase
		Subclass: cytochrome P450, subfamily IVF, polypeptide 3; leukotriene B4 omega hydroxylase; leukotriene-B4 20-monooxygenase; cytochrome P450-LTB-omega
		Subclass: cytochrome P450, subfamily IVF, polypeptide 11
		Subclass: Cytochrome P450 4F12 (CYP1VF12)
		Subclass: cytochrome P450, subfamily IVF, polypeptide 8; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: similar to CYTOCHROME P450 4F6 (CYP1VF6)
		Subclass: cytochrome P-450LTBV

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NM_010286 NP_034416.1	U:(C-HI) 2.83, F:(HI-D) -2.17	Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R)
		Alternate: hypothetical protein DKFZp566A093.1
NM_008362 NP_032388.1	U:(C-HI) 2.59, F:(HI-D) -2.22	interleukin 1 receptor
		Subclass: interleukin 1 receptor, type I
		Subclass: interleukin 1 receptor-like 2
		Subclass: interleukin 1 receptor accessory protein-like 2
NM_019977 NP_064361.1	U:(C-HI) 2.51 F:(C-D) -2.15	unknown protein
		Alternate: aldehyde reductase (aldose reductase) like 6; similar to mouse aldehyde reductase 6 (renal); myo-inositol oxygenase; kidney-specific protein 32
NM_010544 NP_034674.1	U:(C-HI) 2.45, F:(HI-D) -2.47	Indian hedgehog protein (IHH) (HHG-2)
		Alternate: similar to Indian hedgehog protein precursor (IHH) (HHG-2)

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NM_011819 NP_035949.1	U:(C-HI) 2.39, U:(C-D) 2.00, F:(HI-D) -2.52	Growth/differentiation factor 15 (GDF-15); (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)
		Alternate:similar to Growth/differentiation factor 15 precursor (GDF-15) (Placental bone morphogenic protein) (Placental TGF-beta) (Macrophage inhibitory cytokine-1) (MIC-1) (Prostate differentiation factor) (NSAID-regulated protein 1) (NRG-1)...
NM_019641 NP_062615.1	U:(C-HI) 2.29, F:(HI-D) -2.08	stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; stathmin; leukemia-associated phosphoprotein p18
		Alternate: Similar to stathmin 1/oncoprotein 18
NM_010121 NP_034251.1	U:(C-HI) 2.15, F:(HI-D) -2.19	Eukaryotic translation initiation factor 2-alpha kinase 3(PRKRL-like endoplasmic reticulum kinase) (Pancreatic eIF2-alpha kinase) (HsPEK)
NM_011579 NP_035709.1	U:(C-HI) 2.13 F:(C-D) -2.1	hypothetical protein R30953_1
NM_011318 NP_035448.1	U:(C-HI) 2.03, F:(HI-D) -2.37	Serum Amyloid P Component (Sap)
		Alternate: C-reactive protein, pentraxin-related; C-reactive protein

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NM_016847 NP_058543.1	U:(C-HI) 2.02, F:(HI-D) -2.03	arginine vasopressin receptor
		Subclass: arginine vasopressin receptor 1A; V1a vasopressin receptor; vascular/hepatic-type arginine vasopressin receptor; antidiuretic hormone receptor 1A
		Subclass: arginine vasopressin receptor 1B; arginine vasopressin receptor 3; antidiuretic hormone receptor 1B; vasopressin V1B receptor; pituitary vasopressin receptor 3
		Subclass: arginine vasopressin receptor 2
		Alternate: oxytocin receptor
		Alternate: vasopressin receptor type 2
C76314 NP_690023.1	U:(C-D) 2.97 F:(C-D) -2.87	KIAA0432
		Alternate: CDC5-like; CDC5 (cell division cycle 5, S. pombe, homolog)-like; Cell division cycle 5, S. pombe, homolog-like; Cdc5-related protein
NM_011128 NP_035258.1	U:(C-D) 2.35, U:(HI-D) 2.73 F:(C-D) -2.85	lipase
		Subclass: pancreatic lipase
		Subclass: pancreatic lipase-related protein 2
		Subclass: pancreatic lipase-related protein 1

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NM_008239 NP_032265.2	U:(C-D) 2.23, U:(HI-D) 2.15 F:(C-D) -2.79	winged helix/forkhead transcription factor
		Alternate: HNF-3/forkhead-like protein 1
NM_019922 NP_064306.1	U:(C-D) 2.05 F:(C-D) -2.29	cartilage associated protein
AF047725 AAD13720.1	F:(HI-D) -2.06 U:(C-D) 2.35	cytochrome P450, subfamily IIC
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 18; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17; microsomal monooxygenase; flavoprotein-linked monooxygenase
		Subclass: cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 19; mephenytoin 4'-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C8 (CYP11C8) (P450 form 1) (P450 MP-12/MP-20) (P450 IIC2) (S-mephenytoin 4-hydroxylase)
		Subclass: cytochrome P450, subfamily IIC, polypeptide 9; cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 10; mephenytoin 4-hydroxylase; microsomal monooxygenase; xenobiotic monooxygenase; flavoprotein-linked monooxygenase
		Subclass: Cytochrome P450 2C10 (CYP11C10) (P450 MP-8) (S-mephenytoin 4-hydroxylase) (P-450MP)

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AK007530 BAB25091.1	F:(C-HI) -7.8, F:(C-D) -2.61, U:(HI-D) 2.99	N-acetyltransferase 8; kidney- and liver-specific gene product; kidney- and liver-specific gene
		Alternative: putative N-acetyltransferase Camello 2
		Alternative: GLA
		Alternative: kidney- and liver-specific gene
		Alternative: hypothetical protein TSC501 [imported]
NM_007825 NP_031851.1	F:(C-HI) -6.41, U:(HI-D) 5.83	cytochrome P450, subfamily VIIIB, polypeptide 1; oxysterol 7alpha-hydroxylase
NM_015763 NP_056578.1	F:(C-HI) -3.7, U:(C-D) 3.14	Lipin
		Subclass: lipin 1
		Subclass: Similar to lipin 1
		Subclass: similar to Hypothetical protein KIAA0188
		Subclass: lipin 2
X71479 CAA50585.1	F:(C-HI) -3.57, F:(C-D) -2.54, U:(HI-D) 2.82	cytochrome P450, subfamily IVA, polypeptide 11; fatty acid omega-hydroxylase; P450HL-omega; alkane-1 monooxygenase; lauric acid omega-hydroxylase

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NM_009669	F:(C-HI)	Alpha-Amylase
NP_033799.1	-3.13	
	U:(C-D)	
	3.23	
		Subclass: amylase, alpha 2A; pancreatic; Amylase, pancreatic, alpha-2A
		Subclass: amylase, alpha 2B; pancreatic; Amylase, pancreatic, alpha-2B
		Subclass: similar to Alpha-amylase, salivary precursor (1,4-alpha-D-glucan glucanohydrolase)
		Subclass: amylase, alpha 1A; salivary; Amylase, salivary, alpha-1A
NM_007643	F:(C-HI)	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36 antigen (collagen type I)
NP_031669.1	-3.03,	
	U:(C-D)	
	2.05,	
	U:(HI-D)	
	3.33	
AK007264	F:(C-HI)	similar to uridine phosphorylase; similar to Q16831 (PID:g2494059)
BAB24924.1	-2.95,	
	U:(HI-D)	
	2.34	
		Alternate: Uridine phosphorylase
NM_010379	F:(C-HI)	MHC class II histocompatibility antigen
NP_034509.1	-2.87,	
	U:(HI-D)	
	2.37	
		Subclass: MHC class II histocompatibility antigen DQw1-beta chain precursor
		Subclass: MHC class II HLA-DQ-beta-1

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			Subclass: HLA class II histocompatibility antigen, DQ(W3) beta chain precursor
			Subclass: MHC class II histocompatibility antigen HLA-DQ beta chain (DQ4) precursor - human
NM_020564	F:(C-HI)		sulfotransferase family, cytosolic; 2B, member 1; sulfotransferase family 2B, member 1
NP_065589.1	-2.84, F:(C-D) -2.36, U:(HI-D) 2.6		
			Subclass: hydroxysteroid sulfotransferase SULT2B1a
			Subclass: hydroxysteroid sulfotransferase SULT2B1b
NM_032400	F:(C-HI)		G protein-coupled receptor 91
NP_115776.1	-2.79, U:(HI-D) 3.03		
			Alternate: P2Y purinoceptor 1
NM_008495	F:(C-HI)		beta-galactosidase binding lectin precursor; Lectin, galactose-binding, soluble, 1; galectin
NP_032521.1	-2.65, U:(C-D) 2.32		
AK003129	F:(C-HI)		Unknown (protein for IMAGE:2819455)
BAB22589.1	-2.51, F:(C-D) -3.41, U:(HI-D) 3.46		
			Alternate: translocase of inner mitochondrial membrane 17 homolog A (yeast); preprotein translocase

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NM_011596 NP_035726.1	F:(C-HI) -2.51, F:(C-D) -2.34, U:(HI-D) 4.16	TJ6 protein	
		Alternate: ATPase, H ⁺ transporter	
		Subclass: ATPase, H ⁺ transporting, lysosomal, non-catalytic accessory protein 1A, 110/116 kDa subunit; ATPase, H ⁺ transporting, lysosomal non-catalytic accessory protein 1 (110/116kD); vacuolar proton pump, subunit 1; clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit; vacuolar proton translocating ATPase 116 kDa subunit A isoform 1; vacuolar adenosine triphosphatase subunit Ac116; H(+)-transporting two-sector ATPase, 116 kDa accessory protein A1; vacuolar-type H(+)-ATPase 115 kDa subunit	
		Subclass: ATPase, H ⁺ transporting, lysosomal V0 subunit a isoform 4; vacuolar proton pump 116 kDa accessory subunit; vacuolar proton pump, subunit 2; H(+)-transporting two-sector ATPase, noncatalytic accessory protein 1B; ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B; renal tubular acidosis; ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 2 (38kD)	
		Subclass: T-cell, immune regulator 1, isoform a; ATPase, H ⁺ transporting, 116kD; vacuolar proton translocating ATPase 116 kDa subunit A isoform 3; V-ATPase 116-kDa isoform a3; osteoclastic proton pump 116 kDa subunit; T cell immune response cDNA7 protein; specific 116-kDa vacuolar proton pump subunit; T-cell, immune regulator 1; infantile malignant osteopetrosis	
AF193796 AAL09298.1	F:(C-HI) -2.33, U:(HI-D) 3.03	Homeobox protein Hox-C13 (Hox-3G)	
		Alternate: similar to homeo box protein C13; Hox-C13 (Hox-3G)	
		Alternate: unnamed protein product	

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NM_016704 NP_057913.1	F:(C-HI) -2.26, U:(HI-D) 3.29	complement component
		Subclass: complement component C6
		Subclass: similar to Complement component C6 precursor
		Subclass: complement C7
NM_007870 NP_031896.1	F:(C-HI) -2.2, U:(HI-D) 2.24	deoxyribonuclease I
		Subclass: deoxyribonuclease I-like 3
		Subclass: DNase gamma
		Subclass: deoxyribonuclease I
		Subclass: deoxyribonuclease I-like 2
		Subclass: deoxyribonuclease I-like 1
		Subclass: DNL1L gene product
NM_010187 NP_034317.1	F:(C-HI) -2.18, U:(HI-D) 2.55	Low affinity immunoglobulin gamma FC region receptor II-B precursor (FC-gamma RII-B) (FCR1I-B) (IGG FC receptor II-B) (FC-gamma-RIIB) (CD32) (CDW32)
NM_007472 NP_031498.1	F:(C-HI) -2.17, U:(HI-D) 2.38	aquaporin (water channel protein)
		Subclass: aquaporin 1 (channel-forming integral protein, 28kD)

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		Subclass: major intrinsic protein of lens fiber; aquaporin
		Subclass: aquaporin 2; Aquaporin-2 (collecting duct)
		Subclass: hAQP-CD=collecting duct aquaporin [human, kidney, Peptide, 271 aa]
		Subclass: aquaporin 4 C2 isoform; mercurial-insensitive water channel
		Subclass: aquaporin 4 isoform a; mercurial-insensitive water channel
		Subclass: aquaporin 4, long splice form - human
		Subclass: aquaporin 5; Aquaporin-5
NM_010024	F:(C-HI)	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2); Dopachrome tautomerase (dopachrome
NP_034154.1	-2.14, F:(C-D) -2.01, U:(HI-D) 2.28	delta-isomerase; tyrosinase-related protein 2)
		Alternate: tyrosinase-related protein 1
		Alternate: tyrosinase (oculocutaneous albinism IA); Tyrosinase
AF385682	F:(C-HI)	EGF-TM7-latrophilin-related protein
AAK62363.1	-2.04, U:(HI-D) 2.02	
		Alternate: egf-like module containing, mucin-like, hormone receptor-like sequence
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 1; egf-like module containing, mucin-like, hormone receptor-like
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform a
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform b
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform c
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform e
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform d

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		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform g
		Subclass: egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform f
		Subclass: egf-like module-containing mucin-like receptor 3 isoform a
		Subclass: EGF-like module EMR2
		Alternate: lectomedin
		Subclass: lectomedin-3
		Subclass: latrophilin 1; KIAA0786 protein; lectomedin-1; latrophilin
		Subclass: lectomedin-1 alpha
		lectomedin-2
		Subclass: lectomedin-2; KIAA0821 protein
		Alternate: CD97 antigen, isoform 1 precursor; leukocyte antigen CD97; seven-span transmembrane protein
		Alternate: CD97 antigen, isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein
NM_010016	F:(C-HI)	decay-acceleration factor
NP_034146.1	-2.04, U:(HI-D) 2.14	
		Subclass: decay accelerating factor for complement (CD55, Cromer blood group system); Decay-accelerating factor of complement
		Subclass: decay-accelerating factor, splice form 1
		Subclass: decay-accelerating factor 1 ab
		Subclass: decay-accelerating factor 4ab
		Subclass: decay-accelerating factor 3

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NM_023740 NP_076229.1	F:(C-HI) -1.7, F:(C-D) -2.35, U:(HI-D) 2.52	PP3774	
		Alternate: Similar to RIKEN cDNA 1500015N03 gene	
		Alternate: similar to Abl-philin 2	
		Alternate: hypothetical protein MGC2993	
NM_009744 NP_033874.1	F:(C-D) -4.15, U:(HI-D) 2.11	B-cell lymphoma 6 (BCL6) protein; B-cell CLL/lymphoma-6; cys-his2 zinc finger transcription factor BCL5; zinc finger protein 51; lymphoma-associated zinc finger gene on chromosome 3	
		Alternate: similar to Bcl6-associated zinc finger protein	
NM_008245 NP_032271.1	F:(C-D) -2.62, U:(HI-D) 2.05	hematopoietically expressed homeobox; proline-rich homeodomain-containing transcription factor (HEX)	
		Alternate: Similar to hematopoietically expressed homeobox	

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CLAIMS

1. A method of protecting a human subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or
5 from either to a type II diabetic state, which comprises administering to the subject a protective amount of at least one agent which is

(1) a polypeptide which is substantially structurally identical or conservatively identical in sequence to a reference protein
10 which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group consisting of human proteins within at least one of the human protein classes set forth in
15 master table 2, subtables 2A and 2C,

or

(2) an expression vector encoding the polypeptide of (1) above
20 and expressible in a human cell, under conditions conducive to expression of the polypeptide of (1);

where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from
25 either to a type II diabetic state.

2. A method of protecting a human subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state which comprises administering
30 to the subject a protective amount of at least one agent which is

(1) an antagonist of a polypeptide, occurring in said subject, which is substantially structurally identical or conservatively
35 identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtable 1B and 1C, or (b) selected from the group consisting of human proteins belonging to at

least one of the human protein classes set forth in master table 2, subtables 2B and 2C,

(2) an anti-sense vector which inhibits expression of said polypeptide in said subject,

where said agent protects said subject from progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state.

3. A method of screening for human subjects who are prone to progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises assaying tissue or body fluid samples from said subjects to determine the level of expression of at least one "favorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtables 1A and 1C, or (b) selected from the group consisting of human proteins within at least one of the human protein classes set forth in master table 2, subtables 2A and 2C,

and directly correlating the level of expression of said marker gene with the propensity to progression in said patient.

4. A method of screening for human subjects who have a propensity for progression from a normoinsulinemic state to a hyperinsulinemic state, or from either to a type II diabetic state, which comprises assaying tissue or body fluid samples from said subjects to determine the level of expression of at least one "unfavorable" human marker gene, said human marker gene encoding a human protein which is substantially structurally identical or conservatively identical in sequence to a reference protein which is (a) selected from the group consisting of mouse and human proteins set forth in master table 1, subtable 1B and 1C, or (b) selected from the group consisting

of human proteins belonging to at least one of the human protein classes set forth in master table 2, subtables 2B and 2C,

and inversely correlating the level of expression of said marker gene with the propensity to progression in said patient.

5 5. The method of claims 1 or 3 in which the reference protein is of subtable 1A or of a class set forth in subtable 2A.

10 6. The method of claims 1 or 3 in which the reference protein is of subtable 1B or of a class set forth in subtable 2B.

7. The method of any one of claims 1-6 in which (a) applies.

15 8. The method of any one of claims 1-7 in which the reference protein is a human protein.

9. The method of any one of claims 1-7 in which the reference protein is a mouse protein.

20 10. The method of any one of claims 3 or 4 in which the level of expression of the marker protein is ascertained by measuring the level of the corresponding messenger RNA.

25 11. The method of any one of claims 3 or 4 in which the level of expression is ascertained by measuring the level of a protein encoded by said marker gene.

30 12. The method of any one of claims 1-9 in which said polypeptide is at least 80% identical or at least highly conservatively identical to said reference protein.

13. The method of any one of claims 1-10 in which said polypeptide is at least 90% identical to said reference protein.

35 14. The method of any one of claims 1-11 in which said polypeptide is identical to said reference protein.

15. The method of any one of claims 1-14 in which the E-value cited for the reference protein in Master Table 1 is not more

than e^{-6} .

16. The method of claim 15 in which the E-value cited for the reference protein in Master Table 1 is less than e^{-10} .

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17. The method of claim 17 in which the E value calculated by BLASTN or BLASTX would be less than e^{-15} , more preferably less than e^{-20} , still more preferably less than e^{-40} , even more preferably less than e^{-60} , considerably more preferably less than e^{-80} , and most preferably less than e^{-100} .

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18. The method of any of claims 2-17 in which the antagonist is an antibody, or an antigen-specific binding fragment of an antibody.

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19. The method of any of claims 2-17 in which the antagonist is a peptide, peptoid, nucleic acid, or peptide nucleic acid oligomer.

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20. The method of any of claims 2-17 in which the antagonist is an organic molecule with a molecular weight of less than 500 daltons.

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21. The method of claim 20 in which said organic molecule is identifiable as a molecule which binds said polypeptide by screening a combinatorial library.

Abstract of the Disclosure

Mouse genes differentially expressed in comparisons of normal vs. hyperinsulinemic, hyperinsulinemic vs. type 2 diabetic, and normal vs. type 2 diabetic liver by gene chip analysis have been identified, as have corresponding human genes and proteins. The human molecules, or antagonists thereof, may be used for protection against hyperinsulinemia or type 2 diabetes, or their sequelae.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US2004/010191

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	COROMINOLA H ET AL: "Identification of novel genes differentially expressed in omental fat of obese subjects and obese type 2 diabetic patients." DIABETES. DEC 2001, vol. 50, no. 12, December 2001 (2001-12), pages 2822-2830, XP002293068 ISSN: 0012-1797 the whole document	1-18
A	HIDA K ET AL: "Identification of genes specifically expressed in the accumulated visceral adipose tissue of OLETF rats." JOURNAL OF LIPID RESEARCH. OCT 2000, vol. 41, no. 10, October 2000 (2000-10), pages 1615-1622, XP002293069 ISSN: 0022-2275 the whole document	1

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *S* document member of the same patent family

Date of the actual completion of the international search 19 August 2004	Date of mailing of the international search report 31/08/2004
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Luzzatto, E

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CONDORELLI G ET AL: "PED/PEA-15 gene controls glucose transport and is overexpressed in type 2 diabetes mellitus." THE EMBO JOURNAL. 15 JUL 1998, vol. 17, no. 14, 15 July 1998 (1998-07-15), pages 3858-3866, XP002293070 ISSN: 0261-4189 cited in the application the whole document</p>	1
A	<p>ZVONIC SANJIN ET AL: "The regulation and activation of ciliary neurotrophic factor signaling proteins in adipocytes." THE JOURNAL OF BIOLOGICAL CHEMISTRY. 24 JAN 2003, vol. 278, no. 4, 24 January 2003 (2003-01-24), pages 2228-2235, XP002293071 ISSN: 0021-9258 the whole document</p>	1
A	<p>WALDER KEN ET AL: "Tanis: a link between type 2 diabetes and inflammation?" DIABETES. JUN 2002, vol. 51, no. 6, June 2002 (2002-06), pages 1859-1866, XP002293072 ISSN: 0012-1797 the whole document</p>	
T	<p>DATABASE NCBI NIH; cyclin B1 20 December 2003 (2003-12-20), XP002293073 Database accession no. NP_114172 abstract</p>	
T	<p>DATABASE NCBI NIH; Cyclin B2 (Homo sapiens) 23 January 2004 (2004-01-23), XP002293074 Database accession no. NP_004692 abstract</p>	
T	<p>DATABASE NCBI NIH; XP002293075 Database accession no. XP_172630 abstract</p>	

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US2004/010191

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	<p> DATABASE NCBI NIH; Unnamed protein product 30 April 2004 (2004-04-30), XP002293076 Database accession no. BBA92054 abstract ----- </p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2004/010191

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 20, 21
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.2

Claims Nos.: 20,21

1) The molecule to which claim 20 relates is only characterised in that its molecular weight is less than 500 daltons and that it has to be an antagonist of any of the polypeptides listed in tables 1B, 1C, 2B or 2C. This sole feature, however, does not allow the skilled person to understand the scope of the claim.

In order to do that he would have to determine whether any of the numerous compounds disclosed in the prior art falling within the given MW range and used to treat and/or prevent diabetes antagonise the effects of the said polypeptides.

However, many of the proteins listed in the tables have a plurality of effects, yet the description provides no indication whatsoever as to which specific effect should be tested and by which kind of assay. Moreover, many of the said proteins (see e.g. BAA92054.1/NM_033373, i.e. the first protein listed in table 1B) is an unnamed protein for which no function/effect is disclosed either in the application or in the prior art (see printout from the NCBI database (Acc. Nr: BBA92054).

The claim lacks thus clarity to such an extent as to render a meaningful search with respect to its subject-matter impossible. Moreover, the description provides no indication whatsoever as to any compound having a MW of less than 500 d which could be used in the claimed method. Claim 20, thus, cannot be searched at all. The same applies to claim 21 dependent thereon.

2) A further reason for not searching these claims is that they also lack support (Art. 6 PCT) due to the absence of any example of any treatment method falling within the scope of claims 20-21.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.